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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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March 26, 2003, 04:18:30 ; Search time 4821.31 Seconds
(Without alignments)
15096.740 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-702-134-7212_COPY_28000_30500 2501 1 atgtccaagataaaattggc......tatcaatggttgcttcaat 2501 Title:

Scoring table: Sequence:

Perfect score:

2054640 seqs, 14551402878 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database:

gb_ba:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	690 Ory	333 Oryza sati	09 Triticum a	05555 Triticu	07 Triticum a	Triticum	0 Lolium	b Lollum	ATOT4261 LOLLUM pe	5 Orvza s	0 Oryza sa	Phaseolus	3 Lactuca	Phaseolus	7 Citrus	Sequence	_ '	A.thallan		S SOLGINGIII	ABO12856 Nicotiana	3 Nicotian	4 Lactuca	w	7 Nicotian	A.thalian	Š	2 Sequenc	zi :	4 Solanum	8 Nicotian	3898 Lycopers	049899 Lycoper	381 A	532 Phaseolus	1202 Lactuca	F249881 Sorgh	3330 Spinacia c	016084 Nic	58 P.	049900 Lycoper	0471 Pisum sati
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ALIGNMENTS

AC096690 145999 bp DNA linear HTG 08-MAY-2002 Oryza sativa chromosome 3 clone OSJNBa0059G06, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces. RESULT 1 AC096690/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AC096690
AC096690.4 GT:20503077
HTG. PHGS_PBASE2.

Oryza sativa

Oryza sativa

GRANATOLA: Manoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Manoliophyta; Liliopsida; Poales; Poaceae; Shrhartoideae; Oryzae; Oryzae; Oryzae; Oryzae; Oryza, Liu,J., Tallon,L., Gansberger,K., Bull,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K.,

REFERENCE AUTHORS

Kim,M., Overton II,L., Bera,J., Tsitrin,T., Krol,M., Jarrahi,B., Jin,S., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S., Utterbach,T., Feldblyum,T., Tang,Q., Haas,B., Suh,B., Peterson,J., Utterbach,T., White,O., Salzberg,S. and Fraser,C. Cyackenbush,J., White,O., Salzberg,S. and Fraser,C. sequence JOURNAL Orbubilshed REFERENCE 2 (bases 1 to 145999) AJTHUE Buell,R. TITLE JOURNAL Submitsed (22-SEP-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Medical Center Dr, Rockville, MD 20850, USA Medical Center Dr, Rockville, MD 20850, USA	ubmission d (08-MAY-20) Canter Dr, R Canter Lr, R This is a 'we This is a'we The of continue of contin	4002: gap of unknown length 71267: contig of 67265 bp in 71367: gap of unknown length 94679: contig of 23312 bp in 94779: gap of unknown length 122220: contig of 27441 bp in 12320: gap of unknown length 14599: contig of 23679 bp in coatlion/Qualifiers 14599 organism="Oryza sativa" cultivar="Nipponbare" db_xref="taxe" (1500") chromosome="3" clone="OsynBa0059G06"	Anote-"japonica cultivar-group" BASE COUNT 40847 a 32003 c 31335 g 41412 t 402 others ORIGIN QUETY Match Dest Local Similarity 100.0%; Score 2501; DB 2; Length 145999; Best Local Similarity 100.0%; Pred. No. 0; Matches 2501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ATGTCCAAGATAAAATTGGCCCAAGTGAAAACTCAGAACTACATAAATAA	OY 121 AAAACCAFTTCACATATGGATCTGTTGAGGAGGCTGCAAAACTGATTTTGCAG 180 Db 115416 AAAACCCATTTCACATATGGATCTGTGAGGAGGCTGCATGCA

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114936 TACTTAGTTAGCTCGGAGCTAGCTACTAATGGATGATATACTTATGCTAGTTAGAT 114877
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Db 115236 TGGCTGGGTACAAAGAGCAGAGTGGGCTAAGCAAATACCGGGTTGTGGCACCATCCCTTT 115177
                                                     Db 115176 CACATTCACTCGCTCTTGATATCTTTCTCTCTCATGGAAAGAAGAGGATAAGTAATTTA 115117
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AC128647 Oryza sativa chrom PROGRESS ***, 33 u AC128647 AC128647.1 GI:219 HTG: HTGS. PHASE1. Oryza sativa Gryza sativa Gryza sativa Spermatophyta; Mago	Ehrhartoideae; Ory' I (bases 1 to 244 Buell, C.R., Yuan, C Kim, M., Overton II Jin, S., Koo, H., Zi Utterbach, T., Feld Quackenbush, J., W Oryza sativa ssp. Sequence Uppublished 2 (bases 1 to 244	Direct Submission Submitted (20-JUL- Medical Center Dr. Medical Center Dr. More: This is a consists of 33 of is not known and a rib not known and a rubicary. Gaps runs of N, but t This record will as as soon as it is		82716 82805 82805 91215 94297 94346 100520	108199 12948 12948 12948 12948 12948 12949 134077 124171 1411791 15479 15486 15686	
RESULT 2 AC128647 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL REFERENCE	AUTHORS TITLE JOURNAL. COMMENT				
1441 GGCACTGCGACCCCACCTCACCATCCTCCACCAGGACCACGTCGGCGGCCTGGAGG	0y 1621 TCGTCAACAGCGCGCCTCGCTGCTGCTTCTTCCTCTGCCCGGACATGGACA 1680 bb 113916 111111111111111111111111111111111111	OY 1801 TTCAGGCCTTCTCCGACTGGCTTAATCATCGTCACCTGCAACCAAC	1981 ATATATATCTGGGGATTATTCAGTTCCTAGCTACTCCTACATGCTTGCT	09 2101 GCACGTACCCATCTATGATCATGCATGTCCACTATTGTTGGTCGTACGATA 2160	Db 113316 GAGTAATTAATTACTCCAGTTGTTGCTCCATCCATCCATC	QY 2401 TTACCTATATACTATAGCTACCACAAACAAACAAAGAAAG

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DD 110297 TGTGGGCGGAGGGCGCGCGCGCGCCCTCGCCCCCGGGCGCCTCGTCGTCAACG 110356
   109217 ATTGATGCCGGGATAGAGAGAGAGAGAGTTAAGAAGGTAGCTAGGGGGAGAGAGCGAGG 109276
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Corganism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="3"
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Σ	Kamiya,Y. Direct Submitted Submitted Frontier 351-01, J.	/protein_id="waba48239.1" /db_xref="d1:1854637" /db_xref="d1:1854637" /translation="wawvvqobbevvpdaavtiscoteipsoetwpaerspgsvavbel. /translation="wawvvqobbevvpdaavtiscoteipsoetwpaerijplicg-	Query Match 62.7%; Score 1568.2; DB 8; Length 1598; Best Local Similarity 99.6%; Pred. No. 1.7e-230; Matches 1593; Conservative 0; Mismatches 3; Indels Qy 576 GGTGATCCAGGGATGAGTAGTTAGTTAGTTAGTTAGTTAG	696 ATCTCCATCGGTTAATTAATTGATTGATAGCTAGATTATCAACAATTAATGAGCATGGTG [
QY 1561 TCGGCGACACCTTCATGGCGCTCTCCAACGCCAAGTACCGCAGCTGCCTGC	QY 1741 TCACGTGGCGGGCGCTGCTGGACTTCACGCGGCCACCTACAGGGCCGACACGCCGCGCGCG	0y 1921 TACCATTAGCATCGATCCATTAATTAATTAATTAATTACTTGTTCCGGCTTAG 1980 DD 110717 TACCATTAGCATCGATCCATTAATTAATTAATTAATTACTAGTTCCGGCTTAG 11076 QY 1981 ATATAATCTGGCGATTATTTCAGTTCCTAGCTACTCCTACATGCATG	GCACGTACCCATCTATGATCTATATACATGCATGTCGACTATTGTTGGTCGTACGTA	TAAATGTG TAAATGTG TCAGCTTT	QY 2401 TTACCTATATACTATAGCTACCACACAACAACAACAAAGAAGAGAGACACATATGAA 2460 DD 111197 TTACCTATATACTACTACCTACCACACAACAAACAAACA	RESULT 3 OSU50333 LEFE DEFINITION OF YEAR SALIVA GIDDER SACESSION U50333.1 GI:1854636 KEYWORDS

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Location/Qualifiers
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Triticum aestivum.
Triticum aestivum.
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                                                      TTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGGCTGGAGAT
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Submitted (24-JUN-1997) Appleford N.E., Plant Sciences, IACR-Long Ashton Research Station, Dept. of Agricultural Sciences, University of Bristol, Long Ashton, Bristol. BS18 9AF UK
2 (bases 1 to 1451)
Appleford, N.E.J.
Cloning and characterisation of cDNAs encoding gibberellin
20-oxidase from wheat (Triticum aestivum L.)
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                                                                                                            PLN 25-JUN-1997
clone S37E.
                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta;—Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 1451)
Appleford, N.E.
Direct Submission
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/clone_lib="LambdaZapScut"
/dev_stage="germinating grain 3 days at 25 degrees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   836 GGCGGAGGAGAGCCCCGGGTCGGTGGCGGTGGAGCTGGAGGTGGCGCCTGATCGACGT
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20-oxidase,
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/evidence-experimental
/product="gibberellin 20-oxidase"
/protein_id="CAA74332.1"
/db_xref="GI:2222800"
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1559 GTCGACTATTGTTGGTCGTACGATATTATATTATATA 1597
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0; Mismatches 228
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for gibberellin
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/organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Maris Huntsman"
/db_xref="taxon:4565"
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from wheat and

20-oxidase gene

Characterization of a gibberellin its expression in trangenic rice

Youssefian, S.

(sites)

Poaceae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooideae; Triticeae; Triticum.

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2 (bases I to 1343)
Youssefian, S.
Direct Submission
Submitted (04-UUL-1997) Shohab Youssefian, Akita Prefectural
College of Agriculture, Biotechnology Institute, 2-2 Minami,
Obgatamura, Minamiakita-gun, Akita 010-04, Japan
(E-mail:shohab@air.akita-u.ac.jp, Tel:0185-45-2026,
Fax:0185-45-2678)
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                                    AUTHORS
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/translation="MVQPVFDAAVLSGRADIPSQFIWPEGESPTPDAAEEHVPLIDI GGMLSGDPAAAAEVTRLVGEACERHGFFQVVNHGIDAELLADAHRCVDNFTWPLPEK QRALRHPGESCGYASSFTGRFASKLPWKETLSFRSCPSDPALVVDYIVATLGEDHRRL GEVYARYCSEMSRLSLEIMEVLGESLGVGRAHYRRFFEGNDSIMELNYVPPCQRPLET

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/organism="Triticum aestivum"

Location/Qualifiers 1. .1343

/strain="Rht3 Dwarf" /isolate="April Bearded" /db_xref="taxon:4565"

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LGTGPHCDPTSLTILHQDNVGGLQVHTEGRWRSIRPRADAFVVNIGDTFMALSNGRYK SCLHRAVVNSRVPRKSLAFFLCPEMDKVVAPPGTLVDAANPRAYPDFTWRSLLDFTQK HYRADMKTLEVFSSWIVQQQQPQPART"

/gene="wga20" /note="14 a nucleotides" 482 c 408 g 241 t

212

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974 TAACCACGGCATCGAGGCGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTT 1033
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                                                                                                                        GGAGATCCCGTCGCAGTTCATATGGCCGGCGGAGGAGCCCCCGGGTCGGTGGCGGTGGA 868
                                                                                                                                                                                                         GGACATCCCGTCGCAGTTCATCTGGCCCGAGGGCGAGGCCCGACCCCGGACGCCGCCGA 250
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                                         Gaps
                                         36.
    Length 1343;
                                         Indels
  DB 8;
Score 596.8; DB 8;
Pred. No. 8.3e-82;
0; Mismatches 252;
                                                                                                                                                                                                                                                  GGAGCTGGAGGTGGCGCTGATCGACGTGGGGGCGGGG
  23.9%;
                                         Conservative
                   Local Similarity
les 827; Conserv
    Query Match
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

mRNA linear complete cds.

1343 bp for wga20,

Triticum aestivum mRNA AB005555 AB005555.1 GI:2257602

AB005555

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

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GRADIPSQFIWPGGESPTPDAAEELHVPLIDI
FFGQVVNHGIDAELLADAHRCVDNFFTMFLPEK
WKETLSFRSCPSDPALLVDIVATLGEDHRRL
GVGRAHY RRFFEGNDSIMKLNY IPPCQRPLET
FTEGRRRSIRFRADARVVNIGDIFFMALSNGRYK
KYVAPPGTLYDAANPRAY PDFTWRSLLDFTGK
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encoding gibberellin
.vum L.)
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252; Indels 39;
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/evidenceexperimental
/product="glibberellin 20-oxidase"
/product="glibberellin 20-oxidase"
/product="glibberellin 20-oxidase"
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/db_xref="glibberellin 204706"
/db_xref="glibberellin 204706"
/db_xref="sprewellin 204706"
/db
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Pred. No. 7.4e-81;
0; Mismatches 239;
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                /codon_start=1
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74.5%;
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Direct Submission
Submitted (24-JUN-1997) Appleford N.E., Plant Sciences, IACR-Long
Ashton Research Station, Dept. of Agricultural Sciences, University
of Bristol, Long Ashton, Bristol. BSI8 9AF UK
Appleford, N.E.J.
Appleford, N.E.J.
Cloning and characterisation of cDNAs encoding gibberellin
20-oxidase from wheat (Triticum aestivum L.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAY14008 1446 bp mRNA linear PLN 25-JUN-1997 Triticum aestivum mRNA for gibberellin 20-oxidase, clone S39A. Y14008
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Triticum aestivum.
Triticum aestivum.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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                                                        1334 AGACCGGCGCCACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAA 1393
                                                                                                                                                                                                                                                                                                  /clone="s39A"
/tissue_type="scutellum"
/tissue_type="scutellum"
/clone_lib="LambdaZapScut"
/dev_zape="germinating grain 3 days at 25 degrees C"
176. 1273
           677
                                                                                                                                                                                                                733 CTACTACCCGCCGTGCCAGCGGCCGTTGGAGACGCTGGGCCACGGGCCCGCATTGCGACCC
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                                                                                            678 -----GCGGGGCCCACTACCGGGGCTTCTTCGAGGGCAACGACTCCATCATGCGCCTCAA
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/cultivar="Maris Huntsman"
/db_xref="taxon:4565"
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GGCGGTGCTGAGCGGGCAGACGGAG	Db 6 GCAGCCGGTGTTCGACGTTGCTTGTGTGTGGCGACATCCCGTCGCAGTTCAT 65 Qy 830 ATGCCGGCGGAGGAGGAGCCCGGTGGTGGCGGTGGCGGTGGTGGTGGCGGTGGAGGTGGTGGTGGTGGCGGTGGAGGAGCTGGAGGTGGCGGTGGTGGCGGTGGCGGTGGAGGAGCTGGAGGTGGCTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGAGGA	Db 66 CTGGCCGGCGGCGGACCGTCCCCGGACCCACCGAGGAGCTGCACGTCACGTCAT 125	CANCATURE GOOD CONTROLL CONTRO	QY 935 GGGGGAGGCGTGCAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGGC 994 I <th>995 GCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGAGAA</th> <th>Db 246 GCTCCTGGCCGACGCGCACGCTGCGTGGACGCCTTCTTCACGATGTCGCTCCAGGGCAA 305 Qy 1055 GCAGCGGGCGCAGCGGCGCGGGGGAGAGCTGCGGCTACGCAGCAGCTTCACGGGGGG 1114</th> <th>Db 306 GCAGCGCGCGCCGGCCCGGCCAGTCGTGCGGCTACGCCAGCTTCACCGGCG 365</th> <th>QY 1115 CTTCGCGTCCAAGCTGCAGGAAGAGAGACGCTGTCGTTCCGGTACTCATCGGCTGGAGA 1174 </th> <th>Qy 1175 TGAAGAGGCCAGGAGGGCGTGAGTACCTGGTGCGGAAGCTCGGGGGGGG</th> <th>1235 GCGGC 1735 GCGGC 1 1 472 -CGCC</th> <th>QY 1295 GCTGATGGAGGTGCTCGGGGAGACCTGGGCATCGTCGGGGGCCACTACTTCCG 1354 </th> <th>OY 1355 GCGATTCTTCCAGCGCAACGACTCCATCATCACCAACTACTACCCGGCGTGCCAGAG 1414 </th> <th>Ay 1415 GCCACTCGACACGCTGGGCACCGCACTGCGACCCCACCTCGCTCACCATCCTCCA 1474 </th> <th>OY 1475 CCAGGACCACGTCGGAGGTGTGGGCGGAGGGCGGTGGCGCCATCCGCCC 1534</th> <th>QY 1535 TCGCCCCGGGGCGCTCGTCGACGTCGGCGACCTCTCATGGCGCTCTCCAACGCCAG 1594 </th> <th>QY 1595 GTACCGCAGCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCTGGCTG</th> <th>OY 1655 CTTCTTCCTCTGCCGGAGATGGACACGGTGGTGCGCCGCCGGAGGAGGTGGTCGACGA 1714 </th> <th>AT 1715 CCACCACCCGAGGTGTACCCGGACTTCACGCGGGGCGCTGCTGGACTTCACGCAGCG 1774 </th> <th>QY 1775 CCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCCGACTGGCTTAATCA 1828 </th>	995 GCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGAGAA	Db 246 GCTCCTGGCCGACGCGCACGCTGCGTGGACGCCTTCTTCACGATGTCGCTCCAGGGCAA 305 Qy 1055 GCAGCGGGCGCAGCGGCGCGGGGGAGAGCTGCGGCTACGCAGCAGCTTCACGGGGGG 1114	Db 306 GCAGCGCGCGCCGGCCCGGCCAGTCGTGCGGCTACGCCAGCTTCACCGGCG 365	QY 1115 CTTCGCGTCCAAGCTGCAGGAAGAGAGACGCTGTCGTTCCGGTACTCATCGGCTGGAGA 1174	Qy 1175 TGAAGAGGCCAGGAGGGCGTGAGTACCTGGTGCGGAAGCTCGGGGGGGG	1235 GCGGC 1735 GCGGC 1 1 472 -CGCC	QY 1295 GCTGATGGAGGTGCTCGGGGAGACCTGGGCATCGTCGGGGGCCACTACTTCCG 1354	OY 1355 GCGATTCTTCCAGCGCAACGACTCCATCATCACCAACTACTACCCGGCGTGCCAGAG 1414	Ay 1415 GCCACTCGACACGCTGGGCACCGCACTGCGACCCCACCTCGCTCACCATCCTCCA 1474	OY 1475 CCAGGACCACGTCGGAGGTGTGGGCGGAGGGCGGTGGCGCCATCCGCCC 1534	QY 1535 TCGCCCCGGGGCGCTCGTCGACGTCGGCGACCTCTCATGGCGCTCTCCAACGCCAG 1594	QY 1595 GTACCGCAGCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCTGGCTG	OY 1655 CTTCTTCCTCTGCCGGAGATGGACACGGTGGTGCGCCGCCGGAGGAGGTGGTCGACGA 1714	AT 1715 CCACCACCCGAGGTGTACCCGGACTTCACGCGGGGCGCTGCTGGACTTCACGCAGCG 1774	QY 1775 CCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCCGACTGGCTTAATCA 1828
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PLN 15-APR-2001 complete cds.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
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Xu,J., Lange,T. and Altpeter,F.
Cloning and characterization of a CDNA encoding a multifunctional
gibberellin 20-oxidase from perennial ryegrass (Lolium perenne L.)
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Xu, 2. Lange,T. and Altpeter,F.
Direct Submission
Submitted (24-NOV-2000) AG Gentransfer, Department of Molecular
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                                                                                                                                                                                               GCGGCGCCTGGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCTGTCGCTGGA 1294
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GCAGCGCGCGCCGCCCGGCCGGCGAGTCCTGCGGCTACGCCAGCAGCTTCACCGGCCC 365
                                                                                                                   1175 TGAAGAGGCGAGGAGGCGTGGGTGACTTGGTGCGGAAGCTCGGGGCGGAGCACGG
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GGLLSGDREAAASVTRLVGDACERHGFFQVVNHGIDAELLADAHRCVDAFFTMSLQDK
QRALRRPGESGGYASSFTGRFASKLPWRETLSRSGVSBEPDLVVDYTYNTGEDHRRL
GEVYARVCSEMSLILLELESEUGGRAHYRRFFEFGNESIMLINIYPPCQRPNGT
LGTGPHCDPFTSLTLLQDDVGGLQVHADGRNLSIRRRADAPVVNIGDFTWALSDRYGK
SCLHRAVVNSRVPRKSLAFFLCPRMDKVVAPPGTSVDEANPRAYPDFTWRALLDFTQK
                                                       15-APR-2001
                                                                                                                                                                                                                                                                     Xu, J., Lange, T. and Altpeter, F.
Cloning and characterization of a CDNA encoding a multifunctional
gibberellin 20-oxidase from perennial ryegrass (Lolium perenne L.)
                                                                                                                                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-NOV-2000) AG Gentransfer, Department of Molecular Cell Biology, Institute of Plant Genetics and Crop Plant Research, Correnstr. 3, Gatersleben D06466, Germany Location/Qualifiers
                                                         PLN 15-APR-20
complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGGTGTTCGACGCGCGGTGCTGAGCGGGCAGACGGAGATCCCGTCGCAGTTCAT 829
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                                                                                                                                                                                             Embryophyta; Trach
a; Poales; Poaceae;
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418 c 368 g 196 t
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                                             ALO142/6
Lolium perenne clone 4 gibberellin 20-oxidase mRNA, AYO14276
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/protein_id="AAG43042.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236;
                                                                                                                                                                                             Streptophyta; Em
7ta; Liliopsida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 578.4; DB 8
Pred. No. 5.5e-79;
0; Mismatches 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lolium perenne"
/cultivar="Limes"
/db_xref="taxon:4522"
                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1175)
Xu,J., Lange,T. and Altpeter,F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:13625519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="GA 20-oxidase"
                                                                                                                                                                                                               Spermatophyta; Magnoliophyta;
                                                                                                                                                                            Lolium perenne
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                    Pooideae; Poeae; Lolium.
1 (bases 1 to 1175)
                                                                                                            AY014276.1 GI:13625518
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al Similarity 74.4%;
799; Conservative
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                                                                                                                                                      Lolium perenne
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GGLLSGDRBAAARVTRLVGDACERHGFFQVVNHGIDAELLGHARCVDAFFTMSLQDKQ
RALRRPGESCGFASSFTGRFASKLPWKETLSFRSCPSEPDLVVDYIVATLGEDHRRLG
                                                                                                                                                                                                                                                           EVYARYCSEMSRLSLEIMEVLGESLGYGRAHYRRFFEGNESIMRLNYYPPCQRPNETL
GTGPHCDPTSLTILHQDDVGGLQVHADGRWLSIRPRADAFVVNIGDTFMALSNGRYKS
CLHRAVVNSRVPRKSLAFFLCPEMDKVVAPPGTLVDEANPRAYPDFTWRALLDFTQKH
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Cell Biology, Institute of Plant Genetics and Crop Plant Research
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                                                                                                                                                                                                                                                                                                                                                                     8; Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                /product="gibberellin 20-oxidase"
/protein_id="AAG43045.1"
/db_xref="G1:13625525"
                                                                                                                                                                                                                                                                                                                                                                                                    232;
              Gatersleben D06466, Germany
                                                                                                                                                                                                                                                                                                                                                                   Score 568.8; DB
Pred. No. 1.6e-77
0; Mismatches 23
                                                                                                                                                                                                                                                                                                         YRADMKTLEVFSDWIQQGHQPAATTTTT"
417 c 362 q 196 t
                                                        /organism="Lolium perenne"
/cultivar="Limes"
/db_xref="taxon:4522"
                                                                                                                                     /note="GA 20-oxidase"
                             Location/Qualifiers
1. .1167
                                                                                                                                                                                                                                                                                                                      362 g
                                                                                                                                                      /codon_start=1
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Best Local Similarity 74.5%;
Matches 800; Conservative
                                                                                                      /clone="8"
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                Correnstr.
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AXU14277 21001 2128 bp DNA linear PLN 15-APR-2001 LOlium perenne gibberellin 20-oxidase gene, complete cds. AXO14277
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SCLHRAVVNSRVPRKSLAFFLCPEMDKVVAPPGTLVDBANPRAYPDFTWRALLDFTQK
HYRADMKTLEVFSDWIQQGHQPAATTTT"

1 624 c 612 g 422 t
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GEVYARYCSEMSRLSLEIMEVLGESLGVGRAHYRRFFEGNESIMRLNYYPPCQRPNET
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Xu,J., Lange,T. and Altpeter,F.

Xu,J., Lange,T. and Altpeter,F.

Direct Submission

Submitted (25-NOV-2000) AG Gentransfer, Department of Molecular Cell Biology, Institute of Plant Genetics and Crop Plant Research, IPK-Gatersleben, Correnstr. 3, Gatersleben D06466, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Poolaes; Lollum.

(bases I to 2128)
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Cloning and characterization of a cDNA encoding a multifunctional
gibberellin 20-oxidase from perennial ryegrass (Lolium perenne L.)
                                                                                                                                                                                                               1535 TCGCCCCGGGGCGCTCGTCGTCAACGTCGGCGACACCTTCATGGCGCTCTCCAACGCCAG 1594
                                                                                                                                                                                                                                                                                                                                      1655 CTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGCGCCCCCCGCGGAGGAGCTGGTCGACGA 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1715 CCACCACCGGAGGGTGTACCCGGACTICACGTGGCGGGCGCTGCTGGACTTCACGCAGCG 1774
                                                                                                                            818
                                                                                                                                                                                                                                                                                                                                                                                                  878
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                                                                                         1775 CCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAATCA 1828
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join(860. 1341,1436. .2045)
/note="GA_20-oxidase"
/codon start-
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/protein_id="AAG43043.1"
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/db_xref="taxon:4522"
661. .666
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Oryza sativa (japonica cultivar-group) mRNA for GA C20oxidase2, AB077025
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PFVWPNGDARPASAAELDMPVVDVGVLRDGDAEGLRRAAAQVAAACATHGFFQVSEHG
VDAALARAALDGASDFFRLPLAEKRRARRVPGTVSGYTSAHADRFASKLPWKETLSFG
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REFFADSSSIMRCNYYPPCPEPERTLGTGPHCDPTALTILLQDDVGGLEVLVDGEWRP
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SAATPQHYPDFTWADLMRFTQRHYRADTRTLDAFTRWLAPPAADAAATAQVEAAS"
455 c 392 g 152 t
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; iilliopsida; Poales; Poaceae;
Bhrharroiddeae; Oryzae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki, A., Ashikari, M., Ueguchi-Tanaka, M., Itoh, H., Nishimura, A., Swapan, D., Ishiyama, K., Saito, T., Kobayashi, M., Khush, G.S.,
                      CGGAGGAGCTGGTCGACGACCACCACCAGGGTGTACCCGGACTTCACGTGGCGGCGC 1755
                                                                                                                                         1936 TGCTGGACTTCACGCAGAAGCACTACCGGGCCGACATGAAGACGCTCGAGGTGTTCTCCG 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1170)
Matsuoka,M., Sasaki,A. and Ashikari,M.
Direct Submission
Submitted (25-DEC-2001) Makoto Matsuoka, Nagoya University,
BioScicence Center; Furocho, Chikusa, Nagoya, Aichi 464-8601,
(B-mail:makoto@nuagil.agr.nagoya-u.ac.jp, Tel:81-52-789-5225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green revolution: A mutant gibberellin-synthesis gene in rice Nature 416 (6882), 701-702 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                               TECTGGACITCACGCACGCCCACIACAGGGCCGACATGCGCCACGCTTCAGGCCTTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="GA biosynthetic enzyme"/codon_start=1
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Pred. No. 1e-46;
0; Mismatches 344;
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/protein_id="BAB89356.1"
/db_xref="G1:20152207"
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Location/Qualifiers
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1. .1170
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Best Local Similarity 63.77
Matches 676; Conservative
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AB077025
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1696
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                                                                                                                                                                                                                                                                                                                                                    985 CGACATCGGGGGCCTCCTCTCCGGCGACCGCGTCGCGGCCGCCGAGGTGACGCGCCTCGT 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGAGAA 1054
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                                                                                                                770 GGAGGIGGIGITCGACGCGGCGGIGCIGAGCGGGCAGACGGAGAICCCGICGCAGITCAI 829
                                                                                                                                           830 ATGCCCGCCGCAGGAGACCCCCGGGTCGGTGGAGGAGCTGGAGGTGGCGCTGAT 889
                                                                                                                                                                                                                                                                                                     890 CGACGTGGGG--------GCGGGGGGGGGGGGAGGTCGTCGGTGGTCCGCAGGT 934
                                                                                                                                                                                                                                        925 CIGGCCGCGGACGAGAGCCCGTCCCCGGACCACCGAGGAGCTGCACGTCCCGCTCAT
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                                                                    Indels 103;
                      Length 2128;
                                                               261;
                      DB 8;
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                 Score 499.4; DB 8
Pred. No. 6.7e-67;
0; Mismatches 261
                 Query Match 20.0%;
Best Local Similarity 68.4%;
Matches 789; Conservative
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9

Gaps

42;

Length 1170; Indels

QY 1061 GGCGCAGCGGCGCGGGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGGGCGCTTCGC 1120

REFERENCE 2 (bases 1 to 1513) AUTHORS Garcia-Martinez,J.L., Lopez-Diaz,I., Sanchez-Beltran,M.J., Phillips,A.L., Ward,D.A., Gaskin,P. and Hedden,P. TITLE Direct Submission JOURNAL Submitted (12-SEP-1996) Instituto de Biologia Molecular y Celualr de Plantas, Universidad Politeonica/CSIC, Camino de Vera s/n, Valencia 46022, Spain FEATURES 1. 1513 Source /organiam="Phaseolus vulgaris" /Strain="Taylor Horticultural" /db.xref="Laxon:3885" /tissue type="Cotyledons"	CDS 1121269 // Codion_start=1 // Product="qibber=1lin 20-oxidase" // Ab_xref="G1:2108432" // Ab_xref="G1:2108433" // Ab_xref="G1:2108432" // Ab_xref="G1:2108432" // Ab_xref="G1:2108433" //	Ouery Match Query Match Query Local Similarity 61.1%; Pred. No. 2.1e-38; Best Local Similarity 61.1%; Pred. No. 2.1e-38; Matches 551; Conservative 0; Mismatches 333; Indels 18; Gaps 2; QY 926 CCGCCAGGTGGGGGGGGCGCAGGCACGGCTTTACCAGGCAT 985	TTTACHIGACCA 1966GGAGCTG 111111 111 1111111111111111111111111	1226 GGAGCACGGCGGCGGCGGCGAGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCT	QY 1406 GTGCCAGAGGCCACTGGGCACCGGTCCGCACCCCACCTGGGTCCACCTGGTCAC 1465
	QY 1301 GGAGGTGCTCGGGAGAGCTGGTCGCAGCGGCCCACTACTTCCGGCATT 1360 III	183 CGACGTCGGCGCCTCGAGGCGACGGCGATGCCCCCTCAGCCCCCTCCCCCTCCCCCTCCCCCTCCCCCTCCCCCTCCCC	QY 1661 CCTCTGCCGGGAGACGGTGGTGCGCCGGAGGAGCTGGTCGACCACA 1720 Db	RESULT 14 PUG70531 LOCUGUS DEFINITION Phaseolus vulgaris gibberellin 20-oxidase mRNA, complete cds. ACCESSION T/0531 SOURCE ORGANISM Phaseolus vulgaris ORGANISM Phaseolus vulgaris SOURCE SOURCE T/0531 Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;	PREFERENCE (bases 1 to 1513) AUTHORS Garcia-Martinez,J.L., Lopez-Diaz,I., Sanchez-Beltran,M.J., Phillips,A.L., Mard,D.A., Gaskin,P. and Hedden,P. TITLE Isolation and transcript analysis of gibberellin 20-oxidase genes JOURNAL Plant Mol. Biol. 33 (6), 1073-1084 (1997) PUBMED 97299839 PUBMED 9154988

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Conservative
                                                                                                                          Similarity
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                   polyA_site
                                                                                                            Query Match
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PINPUNERCHSKKSKDLPWFLLDLGGFLSGRSSSTKEASKLVGHAQVRHGFLVVNHG
VDAMLISDAQVRADLFFELPLSEKQRAAKAGESCASSFTGRESKLPWKFTLSFR
FSAEKNSADIVKDYFENTMGEEFVRLGKVYQEYCNAMSRLSLGTREELGLSLGFOWRSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toyomasu,T., Kawaide,H., Mitsuhashi,W., Inoue,Y. and Kamiya,Y. Phyrochrome regulates gibberallin blosynthesis during germination of photoblastic lettuce seeds
Plant Physiol. 118 (4), 1517-1523 (1998)
                                                                                                                                                       1115
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   1585
                                                            CAACGCCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCCG 1645
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Lactuca sativa Ls20oxl mRNA for gibberelin 20-oxidase, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAR-1998) Tomonobu Toyomasu, Yamagata University, Reculty of Agriculture; Wakaba-cho 1-23, Tsuruoka, Yamagata 997-8555, Japan (E-mail:toyomasu@tds1.tr.yamagata-u.ac.jp, Tel:81-0235-28-2861, Fax:81-0235-28-2812)
CAICCGCCCTCGCCCCGGGGCGCTCGTCAACGTCGGCGACACCTTCATGGCGCTCTC
                    936 CATCAAACCCGATGTCAATGCTTTGTTGTTGTCGATGTTGGTGATACCTTCATGGCCTCTTTC
                                                                                                                        CTCGCTGGCCTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGCGCCGCCGGAGGAGCT
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Lactuca sativa seed germination seed cDNA to mRNA.
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/db_xref="taxon:4236"
/tissue_type="seed"
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/db_xref="GI:4164141"
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Search completed: March 26, 2003, 14:10:32 Job time : 5400.98 secs

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SUMMARIES

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AC096690 145999 bp DNA linear HTG 08-MAY-2002	Oryza sativa chromosome 3 clone OSJNBa0059G06, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	AC096690	HTG: HTGS_PHASE2.	Oryza sativa.	Oryza sativa	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	permatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	Enrhartoldeae; Uryzeae; Uryza. 1 (bases 1 to 145999)	<pre>Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K.)</pre>	
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ALIGNMENTS

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Kim, M., Overton II, L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B., Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Utterbach, T., Feldblyum, T., Yang, O., Haas, F., Suh, B., Peterson, J., Quackenbush, J., White, O., Salzberg, S. and Fraser, C. Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0059606 BAC genomic
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Direct Submission

Submitted (08-MAY-2002) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA

Wordical Center Dr. Rockville, MD 20850, USA

WOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* are represented as runs of N. The order of the pieces

* are represented as runs of N. The order of the pieces

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and
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1368 94679: contig of 67312 bp in length
1368 94679: contig of 23312 bp in length
1368 94679: contig of 23312 bp in length
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Submitted (22-SEP-2001) The Institute for Ge
Medical Center Dr, Rockville, MD 20850, USA
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/db_xref="taxon:4530"
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	36023: contig of 36072: gap of un 36072: gap of un 50772: contig of 50772: contig of 57039: contig of 66111: gap of un 66062: contig of 82755: contig of 82755: contig of 91263: gap of un 91214: contig of 94296: contig of 94345: gap of un 94345: gap of un 100470: contig of	unknown of 7830 unknown of 21287 of 21287 unknown of 4542 unknown of 13006 unknown of 18026 unknown of 2929 unknown of 2929 unknown of 2929 unknown of 2929 unknown of 18026 unknown of 18026 unknown of 5135	193576: gap of unknown length 195576: gap of unknown length 199224: contig of 3084 bp in 199224: contig of 3084 bp in 1992272: gap of unknown length 204906: contig of 5634 bp in 120456: gap of unknown length 210165: gap of unknown length 212166: gap of unknown length 212169: contig of 2003 bp in 1216130: contig of 3914 bp in 1216130: contig of 3314 bp in 1216130: contig of 2333 bp in 1216138: gap of unknown length 218559: gap of unknown length 221079: gap of unknown length 221079: gap of unknown length 221079: gap of unknown length 2226395: contig of 5316 bp in 1221079: gap of unknown length 226395: contig of 5316 bp in 1221079: gap of unknown length 226443: gap of unknown length 226443: gap of unknown length 226443: gap of unknown length 229778: contig of 3335 bp in 1
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1045 185252: gap of unknown length
18553 195534: contig of 10102 bp in length
5553 195402: gap of unknown length
5513 19666: contig of 3214 bp in length
5613 19666: contig of 3214 bp in length
18665 207376: contig of 8712 bp in length
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Submitted (1-DEC-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 207376)
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Submission
Submitted (02-APR-2002) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
on Mar 5, 2002 this sequence version replaced gi:18767486.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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Oryza sativa chromosome 3 clone 0J1754_E06, *** SEQUENCING
PROGRESS ***, 34 unordered pieces.
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10151: gap of unknown length
13105: contig of 2954 bp in length
13154: gap of unknown length
20540: contig of 7386 bp in length
20589: gap of unknown length
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Beet Local Similarity 99.7%; Pred. No. 0,	Db 21623 TCAAATGKTAGTCGAAAAGTCAATGG	21563		Oy 1201 GGTGCAGCTGAATGAGAGGTGAAGG	1261	QY 1321 CAGCGAGGTCCCAAGATTTGCAGG7 [Qy 1381 CATCCGCCCAAGAGGACGCCGAGT 	1441	1501	QY 1561 CCAGGCCCAGCTCAAGGATCTGGAGG			1741			1921	1981 TTTCTARGCTTC 1981 TTTCTARGCTTC 1 1 1 1 1 1 1 1 1	Oy 2040 GARAGGTTTT 2050 DD 20603 GAGAGGTTTT 2059	RESULT 4 CNSO8C7Q
\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	<pre>ilarity 99.7%; Pred. No. 0; Conservative 3; Mismatches 2; Indels 1; Gaps</pre>	CGTCGTTCGTTTTGTGCATCCATCCAGAATTCGTTCCAGATCCAGCCAG	AAGCTTCTCTCTCTGTTATTAAGAGCAAGCAAACAGTAGTCTAGCGAAGCGAGACT 	GCGAGAGCAGCATTGTTCTTCTCTAGCTATTAGTGGTGGGGAATAATGGCTCCCG	CCACCACCGCAGCAATGGCCCTCGCGCCGCCTCCTTCCCATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCACACATCA	TCAAGCAGCTGCAGCTCCCCCGTCTGTCTCCGTCTCCGTGCCCCTCCGCTCCGGTTTTC	TJGGCCGCGCACTGCCTGCTGCTGCCACCACAGCCGCTGCTCGCCGCGAGAGCCGCC	GCAGCAGCGCGTGTCCGTGCGGALGTCGTGGGACGGGCCCCTCTCCTCGGTCCGCCTCA	421 TTATGCAGGCCGCAACGTCAAGGTTCTCCTCTCCTACCACCACTACCTTGCTTG	481 TGGAATTICCTTCGTTTCATATTATAAGGTTTTCTAGCATTACTCATATTCACATATATA [541 TATATAIGATAATATTCTAGATTCATTATCATATATATATATATAGTAATGCTAGAAAA	TCTTATAACCTGAAACAGAGGAGTATATAATTCGGTAATGGAACTAGAGTATTTGTT 660	661 TTATTAATTGGACCTTTATGAAATACTAGTAGAATTCAACGAAACTACATCTTCTTAT 720	721 TGGTTATATTAGTAGTAATTTGCTTCACTAGAATTCTATTTTATACTAGAGAGATTAAAA	781 ATTATTACAAAACTAACTGTATACCCGTTGCAACGGAATAGTAATATGGACTATTACTT	841 ATTACTACCTCCATATTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCAT	901 TCGTCTTATTAAAAAATTATGTATCTATTATTATTATTATTATTATGATTCGTCAT	961 CRAATRITITTRAGCATGACRIAAACATTITCATATTIGCAAAAAAAAAAAAGGATGG 	1021 TCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATATGGG
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TCCTGTACAAGAGGAAGGAAGGAGGCTTCGGTCTCA 20784 TACACCTCCTGCATCACCATCCTCATTGCTAATTA 20664 21324 SGTGTCATACATTAAAATACGGAGGATTATATGGG 21564 3GAGCACATCGAGGAGAAAGGCGGGGAGAGCAGTGGC 21384 1260 STCCACCTACGCCAGCATCGACCTCGCCTCCTCCAT 1440 CAAGGAGAAGGACCGACGTCCGCCACCTCAAGGG 1500 SCCGCCATCATTGCTCGACAACAACGACGACGACGC 1560 SGAGGCCGTCGCCGCGGACGACGACGCACGGTGCT 1620 IGATCAAIGCAIAIAAAICAAAICAITCAIGAACCA 1680 TAGTGAATGTGGACCACAACTTCTACGCCTTCAGAG 1800 TCCTGTACAAGGAAGGAAGGAGGCTTCGGTCTCA 1860 rccacaagaagaccarcccaacrcraccaccacc 1920 TACACCTCCTGCATCACCATCCTCATTTGCTAATTA 1980 STGCGAGATCACTCTCTCACCAAGCGCCACGGCGT 1380 SGTGGACGTGCGCCTCTCCGCCGCGGGGGGGGGT 1320 FGGAATGGAATGAAAGCGTACGTGCGTGGCGTGGC SGAGCACATCGAGGAGAAGGCGGGGAGAGCAGTGGC

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source
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and Genoscope sequencing data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
  HTG 29-APR-2002
                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Manoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryzae; Oryzae; Oryzae; Oryzae; Oryzae; Origede, Coriede, G., Cattolico, L., Demange, N., Wincker, P., Segurens, B., Pelletier, E., Scarpelli, C., Salanoubat, M., Weissenbach, J. and Quetier, F., Scarpelli, C., Salanoubat, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (29-APR-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contigs composition:
2400 by contig from 1 to 2400
6009 by contig from 2501 to 14059
11245 by contig from 8610 to 14059
11245 by contig from 14160 to 25404
85465 by contig from 12505 to 110969.
* NOTE: This is a "Vorking draft' sequence. It currently consists of 5 contigs. Gaps between the contigs.
* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and the accession number will be preserved.
* This sequence will be preserved.
* 2401 2500: gap of 100 bp in length
* 2401 2500: gap of 100 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Web : www.genoscope.cns.fr) IMPORTANT\colon This \ sequence \ is \ unfinished \ and \ does \ not \ necessarly \ represent \ the \ correct \ sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                   Oryza sativa chromosome 12 clone Monsanto-0J1298_D03, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 110969;
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linear
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  DNA
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a 25445 c 24509 g 30381 t
                                                                                   AL731741.1 GI:20160276
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
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/sub_species="japonica"
/db_xref="taxon:4530"
110969 bp
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                                                                                                                                         Oryza sativa.
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KEYWORDS
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842 TTACTACCTCCATATTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCATT 901

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Clone:10429204

Dublished Only in Database (2001)

E Sasakir, "Amsteunoto,T. and Yamamoto,K.

Direct Submission

Direct Submission

Direct Submission

Bubartia (17-MAY-2001) Takuji Sasaki, National Institute of

Submitted (17-MAY-2001) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

May 24, 2001 this sequence version replaced gi:14575596.

On Awy 24, 2001 this sequence version replaced gi:14575596.

On Awy 24, 2001 this sequence version replaced gi:14575596.

Genes were predicted from the integrated results of the following:
GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor

(October 1998 version). The genomic sequence was searched against

NCDI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at

RGP. Protein homologyse of the coding regions were searched against

NCDI NonRedundant Protein database with BLASTP2.0. ESTS represent

the identified cDNA sequences using BLASTP 2.0 with the

corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is

classified based on the protein name to indicate the homology level

such as same name, 'putative-' and '-like protein'. A gene without

significant homology to any protein but with BST homology to any protein in

slings the entire length of partial sequence) is classified as an

'unknown' protein. A gene predicted with a gene prediction program

is classified as a hypothetical' protein.

A gene redicted with a gene prediction program

is classified as a hypothetical' protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLN 21-MAR-2002
chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.daa.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    olone:P0459B04.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceāe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The orientation of the sequence is from SP6 to T7 of the PAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
95874 ITATAGCCTCCATATITTAAIGTATGACACCGITGACTTTTTGTCCAACGTTGACCATT 95933
                                                                                                                                                                        95993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95994 AAAIGIITITTAAGCATGACATAAATATTTTCATATTTGCACAAAAATTTTGAATAAAAC 96053
                                                                                                                                                                                                                                                            AAATATTTTTTAAGCATGACATAAACATTTTCATATTTGCAAAAA.-----AAAAAAAC 1014
                                                                                                                                                                                                                                                                                                                                                                                                                           1015 GAATGGTCAAATGTTÄGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTA 1074
                                                                                    Sasaki,I., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0459B04
                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
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PTCFNVVLEQPYQBG"
join(65394. .65405,65622. .65777,66253. .66420,66764. .67036)
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PLIEKSETVNHSYMNNEYGSSMDEQRATESEDEQRMEREOBIVMASALSCLFYFYCDG
GKIIRSKALGGLDIRVIKTLLEISVEHSWAKVVHSKLICMÉTNHLYQSDGAPNGADTO
HFLPDQIDPYGGYDYICLESTSRANSREKRDLFFVLEDYVLHQINBTFLAGGISTYTY
DDAQPLASLLAGADAPEAFYISVKHGVEGYGDMLRKAISSALSQSTEYEQINVLLDKV
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SSFKGGLSSAMGSFSRIGKGSGRLVVDGSSVGELANKPDHDFSSYAAAALICDT"
complement(join(56259. 56384,57157. 57234,57351. 57401,
57550. 57550,58700. 58869,59089. 59518))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(56259. 56384,57157. .57234,57351. .57401,
57530. .57550,58700. .58869,59089. .59518))
/gene="P0459B04.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPPLFSAPALHRRRLLRHAAAFALVLLAVALLFLLLVHPRSLGT
PSPSPSYGHRLPTLVDLTLVHGAKEKGAVCLDGTPPGYHWLPGFGDGSNKWLLHLEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWCRNRTSCDHRKKTSLGSSAYMETRVEFVGILSDDKAQNPVTIPYTPHFTSPHFLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STVLRRHSLQYGATFFFRGQRIWFAVWAELLPKGLARAKGGRHFWEKDLRKRFPGGSS
DMEPGQCFFPQEVAKGITTPWFILNPAYDVWGTVABAYGDWFFDRREVKEIDCEYPCN
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/translatin="MAVQYQESKRDIIANPA
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SPSLVKSLNYVRSLVARHIPKLSFQPIGHSVAPTSTKQSLPSLSSFFNKSLVSQLTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id~"BaB63825.1"
/db_xref~"GI:15290134"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDRFTALHTAAANGRLQVLSMLLDRDGDVDVLSRKRGFPLMVAAMRGNTECVVRLLRG
GANVLTFDSPRARTCLHHAAYYGHAECLQAILGAAAQAQGPVAASWGFARFVNVRDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWGADRLQRDSAGRIAYAVAMRRGHRACAALLNPAAAEPIVWPSPLKFIGELEADAKA
LLEAALMEANREREKRILHGSDINIKGGDEEEESEDEBEACNICFEQACSMEVKECGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STŘESSNDFADLODFHTQGFLEVGAAALLVGDMEAKINDQQWKYSFIQDFPDIDELQP
STSTASTFASSQSHLKAITASKRMKSGPNQVCEQQPLKINPABISEVIAEVCSETTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRKIDGTVSTFSRIDTEFAYMIQVTKSYKCFSSIRDGHEDADVALRARLCWATLHSLL
NSQISSYRHHGYIMLVELLLSEISEETDGSIWSKIQKLQDEIEVAGSQDLSSSEVSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCLLCGLLKSKHNFIRWGFLYVLDKFLMRCKLLLDDNDMQEHTVADHSKHRLDKAFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDIMNSALLLIVVQNNETDHINILKMCDMLFSQLCLRLPSSNVMHMGGLQSLGQLFGCT
TKNIESHLETLASHQNVGNKNFCRSEFLQDISVNQTAQFTLLSETSMAALLLRGLAIA
                                                                                       /translation="MSCCGGNCGCGSSCOCGNGCGGSIDRCNSNLTIDICRCKYSEVE
                                                                                                                           PTTTTTFLADATNKGYVWCCFRRIRDGGGERQLRLQHLQVRHQLRLLLLQLQLEETYL
                                                                                                                                                HPIRHLINELPVPLHMPCTSYLACMOVINILIAS"

complement(join(39014, .39084,40410, .40797,41574, .42182,
427266, 43001,43510, .43798,44035, .44145,44725, .44905,
45677, .45835,46704, .46958,47100, .47606,47693, .47743,
47836, .47915,48207, .48236))
                                                                                                                                                                                                                                                                                                                                           complement(join(39014. 39084,40410. .40797,41574. .42182,
42726. 43001,43510. .43798,44035. .44165,44725. .44905,
45677. .45553,46704. .46958,47100. .47606,47693. .47743,
47836. .47915,48207. .48236))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AITNMDLVESKESHAPSDLISSATEKADGGEPADDTKYISFDILNWRWHVYGERQASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATPLHLAARHARASCVRLLLDKGAIVSAPTAVYGFPGSTALHLAARAGSMECIRELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMQLVARVPTSLFFWPLMQLEGAASDDIALGIAVGSTGSESPVTCKLITGSKRCGYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similar to Arabidopsis thaliana chromosome 3, T2E22.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="putative receptor-like kinase Xa21-binding
protein 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0459B04.7"
/note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB63826.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/protein_id="BAB63824.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:15290135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53255. .54595
/gene="P0459B04.8"
53255. .54595
/gene="P0459B04.8"
                                                                                                                                                                                                                                                                                                             /gene="P0459B04.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(29581. 30063,31083. 31412,32281. 32354,32618. 32708,32819. 32911)
//gene="P0459B04.4"
join(29581. 30063,31083. 31412,32281. 32354,32618. 32708,32819. 32911)
//gene="P0459B04.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start_1
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/brotein_id="sab63821.1"
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ASGDPSPPRAEGGGNPLIAURRTLIBPLGDYGFGRKSWYMSGGGVLLALALA
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EVEDDKIIVPRNSVVBVNOSGLIAMETLIDITPKDPLPFPSVGPLDPDCSKEGLILLODY
EVEDDKIIVPRNSVVBVNOSGLIAMETLIDITPKDPLPFPSVGPLDPDCSKEGLILLODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERMKGQQVSUDALVGIFTRLGRDMEEIGVHKSYKLAEKVASIMERAQPLLSRVRDSD
LVKDVEI IAKGLADASGDLRRLKSSMLTPENTDLIKQSIFTLIFTLKNIESISSDISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAHSGFSGSLTSPRFDLAVDMGHPFLNRTVDGFLKIGAKNAMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                            AVCVŠKWOGFDKIPGSDHEYIDVIMNSDTEYRLIIDIDFRSHFEIARAVDSYDSLLNS
LPVYYVGTLPRLKQFLHVWYDAAKWSLKQNSMPLPPWRSLPYLQAKWHSKYERIDIHI
BQDFHSTASDHALCIGHLKRLKSSLQSELDTERLLMMPIKTDWKRRAKFERRRRSLL
                                                                                                                                                                                                                                                                                                                                                     /translation="MLLAKELGLSPPAAVTPRRRPPPARVPASPSGGSPVAVGDLWLR
                                                                                                                                                                                                                                                                                                                                                                                   TKGAGGGGGFGSHSHESEMDLAMLYTDFLENGGTGGADSRASSDSDSALSDHLADNI
SIYKQGGDEKENELLSMYHSLLFSIHESDLLAFKRGQCSASCIRHLLVKLLRYSGYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //orte="contains ESTs AU031375(E61447), AU029988(E50438)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein
similar to Arabidopsis thaliana chromosome 3, MQC12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15732. .16972
/note="5" IIR"
/note="5" IIR"
/note="045804.2"
17059. .23204
/gene="045804.2"
/fene="probably inactive due to frameshift(s) in CDS probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note≈"probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similar to Oryza sativa chromosome 6, P0644B06.8"
                                                                                                                                                      /note="contains EST D47569(S13151)
similar to Arabidopsis thaliana protein F12L6.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAVTGALVSAASNSHRONVVKNAITGGAIATAAEFLNYLT"
join(36642. .36706,36726. .36840,36947. .37177)
/gene="P0459B04.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(36642. 36706,36726. 36840,36947. 37177)
/gene="p0459B04.6"
                              .7448,7556. .8040)
                                                                                          .8040)
                    FTGDDATRRNIKLLIKSLSRLL"

join(33620. 33733,35242. 35382)

'gene-"Pod459B04.5"

join(33620. 33733,35242. 35382)

'gene-"P0459B04.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P0459B04.3"
/note="nrch."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(23838. .26976)
/gene="P0459B04.3"
complement(23838. .26976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB63822,1"
/db_xref="GI:15290131"
                                                                                                                                                                                                                                                                                      /protein_id="BAB63820.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar to polyprotein"
                                                                                                                           'qene="P0459B04.1"
/clone="P0459B04"
                                                                                                                                                                                                                      unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="3' rm-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pseudogene
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27447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /bsendo
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This sequence of P0698H10 clone has an overlap with P0518C01 (DDBJ: AP003277) clone at the position 1 to 80,700 of 5' end and with P0459B04 (DDBJ: AP003627) at the position 103,811 to 153,449 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.

Location/Qualifiers
1..153449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB89859.1"
/db_xref="G1:20160923"
/translation="MEBEBEBEBEBEKERKKERVVELISMEDERWKLSSSKGRSKSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WFERRLSFRLRSCCCFFFFLLVVVVVVVIAMMYQTQAVGTNDIDQAGETWFLDEGPAS
RAEEQRPAGATCICSLLARAYCRPCLRWHACTTYYCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLAKQCNAMQSDQIFWRMKDEVTRALGRILSGVGRVTNDTRLAW
LAMRYFSANNPLLAPIFFGKLKQHCWMADLLLKRGINSHSAYPFYAQELETANHILLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLLLQRTYBATKELKNKLASYLFLIDRFFFFFFFFFFFFTUSLTSCYYRDIPGLPQ
RWMHAKKASRIDAVGGINQIQSRILRASIRYDMYADRSMLPASCVRTYSIYCTYYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(26367. 26488,26778. 26908,27759. 27874,
28412. 28548,29329. 29416))
/gene="P0698H10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MQTLMSVFVIIIGNYTAIDWITDIVIFWIGVGTWHLKRCQTVKL
XIAAPLIFYIVMALFGFIKQLIEYNIIAFCHPSTVFRFGKSTRETWTKMIEALGFGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MHAGIDRFKFSCDVLLAANSQDILCIVMLAWRRASHAYVVLSSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHCSIQYYRVGVVICSHIGSISINHMYHNSTPNYKY"
complement(join(26367. .26488, 26778. .26908, 27759. .27874, 28412. .28548, 29329. .29416))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(32396. 33552,33673. 33814,34064. 34197, 35201. 35214,36092. 36171))
/gene="P0698H10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .16340,16376. .16523,17419. .17541,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .33552,33673. .33814,34064. .34197,
                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(4643..4651,4721..4846,4888..5021,8292..8312,9406..9448))
/gene="p0698H10.1"
                                                                                                                                                                                                                                                                                                                                                                     .4651,4721. .4846,4888. .5021,
                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(11376, 11773,12758, /gene="P0698H10.2"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(11376. .11773,12758. /gene="P0698H10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(32396. .33552, 35201. .35214,36092. .36171))
/gene="P0698H10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(16198. .16340.
19928. .19954,20609. .20764))
/gene="P0698H10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
/codon_start=1
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                               complement(join(4643. .46)
8292. .8312,9406. .9448))
/gene="P0698H10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAB89860.1"
/db_xref="GI:20160924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB89858.1"
/db_xref="G1:20160922"
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                                                                                                                                                                                                                                                                                                                                        /clone="P0698H10"
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                                                                                                                                                                                                                                                                                                                 /chromosome="]
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                                                                                                                                                                       FEATURES
/gene="P0459B04.10"
join(65394. .65405,65622. .65777,66253. .66420,66764. .67036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the identified CDNA Sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein.' A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLN 17-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, UKL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Faz:81-298-38-7463, On Apr 16, 2002 this sequence version replaced gi:16416398. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTNZ.0, as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NORSEQUADANT Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryzaeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 1,
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                                                                                                                                                                                                                             44550 AAACGAATGGTCAAACGTTGGTCGAAAAGTCAACGGCGTCATACATTAAAATACGGAGGG 44609
                                                                                                                                                                                                                                                                                                                                                                                                                   CATCAAATATTTTTTAAGCATGACATATATTTCATATTTGCAAAAA-----AAAA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1011 AAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGG 1070
                                                                                                                                                                                                                                                                                                     838 CITALTACTACCICCATALTITAAIGIATGACGCCGTTCACTITITGICCAACGITTGAC 897
                                                                                                                                                  Gaps
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Direct Submission
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0696H10
                                                                                   DB 8; Length 142475;
                                                                                                                                             7;
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Oryza sativa (japonica cultivar-group) genomic DNA,
PAC clone:P0698H10.
                                                                                                                                          0; Mismatches 24; Indels
                                                                                Score 190.6; DB 8
Pred. No. 1.1e-22;
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2 (bases 1 to 153449)
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                                                                                   8.7%;
                                                                                                                                             Conservative
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                                                                                                                Similarity
                                                                                                                                          Matches 222;
                                                                                      Query Match
                                                                                                                   Local
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AP003298
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SOURCE
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/translation="MVLRPRQWRRRSLRTALAASYYVLCGSDVPAGVPYTYDVALLL
LVALIFSTLSPSEAEAAAAATSTNLRRRQEVQSLLRRLNKPPLATIQSPDGDIIDCV
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                                                                                                                                                                    RAISŸAIFCKKTHGSHHPÄLAGYTDGHHQYGVÄSATĞDANYYGTKAIINIMQPTIATS
GDFGIAAQIATISAGSYQNKULNYITAGMOYYPALYRDEKTRFIYMTRDAYDQTGCYNL
ACSGFIQTNTVIGGSTSPVSIYGEQYEYDYLVWKDLAGGNWWLQVQGKYVGYWPSSI
FTHLQTGYADTYPWGGSFUNSPESGTPPMGSGHPPKEGFEGKATYSKAIQVVDSSNKIKSP
NGVSLIAPLPNYINVWIGSSSTTSWGTYIYYGGSGCP"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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Buell, C.R., Yuan, Q., Moffat, K.S., Hill, J.N., Burr, P.C., Hsiao, J.,
Zismann, Y., Pai, G., Bowman, C.L., Fulli, C.Y., Vanken, S.E.,
Bowman, C.L., Craven, B., Utterback, T.R., Khalak, H., Feldblyum, T.V.,
Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.
Oryza sativa chromosome 10 BAC OSJNBa0026012 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 148220 CITAATACTACCTICATATITTAATGTATGACGCGGTGACTITTGTCTAAACATTGAC 148279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 148340 CATCAAATGTTCTTTAAGCATGACATAAATATTTTCATATTTGCACAAAAATTTTGAATA 148399
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Submitted (13 MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
5 (bases 1 to 165279)
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                                                                                                                                                                                                                                                                                                                                                 Length 153449;
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                                                                                                                                                                                                                                                                                                                                                                                                       24; Indels
                                                                                                                                                                                                                                                                                                                                                 DB 8;
                                                                                                                                                                                                                                                                                                                                              Score 190.6; DB 8 Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
/codon_start=1
/protein_id="BABB9866.1"
/db_xref="G1:20160930"
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join(42534. .42746,42822. .43280,43389. .43616,44080. .44259,4335. .44655,44769. .44834,45256. .45308,45405. .45491)
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                                                                                                                                     STTSPPACLRRRIJVSSPMRLVGHTTVHGRPRLHRPAGLRRRIJVFPPARLAYYAAAI
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                                                                                                                                                                                                                       PFMGVHVFADRLARAAADWCFRLHGWPIMPPLLIDVYDFTAGLPPSPPTGVLAYTVGWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSFSIQQQQHDDDQLLQPAADDHLAVQAPPDDCYNINGSSSSGLAMSLDDDBQAAGAG
GLLEDVVPLLVRRPPPPICNNNNYYYSPATTCTSDNEYGSSASASPSSSVSWSSWTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKTPHKVLDAPSLQDDFYLNLVDWSSQNTLAVGLGNCVYLWSASNCKVTKLCDLGPRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQILVWNQRSQQPILRLTBHTAAVKAIAWSPHQQGLLASGGGTADRCIRFWNTVNGNM
LNSVDTGSQATCEHSWVFPRPNHGVEVPITVRGCYSNWTHAASALPCNVTTIVTGAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIEKLGVEESISLELCVLLYKQYGTTNAGLRAVGYQFDYDDFHSYVHGRLAYEKIRPD
PVLRNILLSLPIRKVVYFNCFDQVFTNGDRIHASRALKRLGIEDCFERVVCFETLNPS
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LLLIAALRPKLIDAHDVSKPRHHDTAVIYYVFTDRPLRPPPTGVSACTAGLLCRRCWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAACDHOLLADGHNFAASSCSPVVFSPEKTLSKTMENKYTLKMKSCGNNGGLADDGYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WRKYGGKSIKNSPNPRSYYRCINPRCNAKKOVERAVDEPDTIJVTYBGLHHHTYTYSHF
LHSISSSSSSTTTQQQLQPQPQMTNCKKKPKLHLHPLLHDDPPPPPPPBMTYMAIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HALESLHNNKEALPELMDEAVKDEDVRKSSKVGIETSVIA."
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49503. 49658)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains ESTs D15121(C0112),C97914(C0112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSPCIDMAILSNIF"
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dene

CDS

gene

CDS

REFERENCE

COMMENT

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complement(join(36223. .36759,36892. .37157,37825. .37996))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMVLMQGGGDQMISGSGVHCSNNDNSGSSSALLNLTMLQYSFLEHRPTGDDMAVGAHF
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41836. .56291
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complement(43917. .43952)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="similar to NAM GB:CAA63101 GI:1279640 (Petunia x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative NAM (no apical meristem) protein"
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33907. .33945
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                                                                                                                                                                                                                                                                                                                                                                                                           complement(34290...34356)
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34452...34525
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complement(36223. .37996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                   Genes were identified by a combination of several methods: Gene prediction programs including Genscan and Genscan (Chris Burge, http://CCR-081.mlt.edu/GENSCAN.html), GeneMarkHaM (Mark Burge, http://CCR-081.mlt.edu/GENSCAN.html), GeneMarkHaM (Mark Burge, http://genemark.biology.gatech.edu/GeneMark/), Figenesh (http://genemark.biology.gatech.edu/GeneMark/), Figenesh (http://www.softberry.com/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tdi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after with EST similarity are named as unknown proteins Genes without proteins ones without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by hypothetical proteins dense sencoding tRNAs are predicted by ENAscan-SE (Sean Eddy, thtp://genome.wustl.edu/eddy/FRNAscan-SE); Simple repeates are identified by repeatmasker (Arian Smit, http://erearcan.edu/eddy/FRNAscan-SE);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:4803672 (Homo sapiens)"
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                                                                                                                               Buell, R.
Direct Submission
Submitted (03-JUL-2002) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
On Jul 3, 2002 this sequence version replaced gi:13129494.
Address all correspondence to:rice@tigr.org
                    Direct Submission
Submitted (29-Ang-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
6 (bases 1 to 163279)
                                                                                                                                                                                                                                                                                                                          BAC clone OSJNBa0026012 is from Oryza sativa chromosome 10 The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This BAC overlaps with rice BAC OSJNBb0044B19 (AC078893) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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Location/Qualifiers
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FEATURES

CDS

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AC092075 164852 bp DNA linear HTG OB-MAY-2002 Oryza sativa chromosome 3 clone OSJNBa0017N12, *** SEQUENCING IN PROGRESS ***, 9 ordered pieces.
                                                                                                                                                                                                                                                                             were identified by a combination of several methods: Gene prediction programs including Fegenesh (http://corw.softberry.com/), genesan (http://corw.softberry.com/), genesan (http://corw.softberry.com/), fenemark.biology.gatech.edu/GeneMark/), tRNMscan.SE (Sean Eddy, http://genemark.biology.gatech.edu/GeneMark/), tRNMscan.SE (Sean Eddy, http://genemark.biology.gatech.edu/GeneMark/), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://nchi.nlm.nih.gov/blast/db) and the EST database at NCGR.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
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                                                    Organ sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC clone: OSJNBb0020011.
On Jul 12, 2002 this sequence version replaced gi:17998510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 101102 AATATTCTTTAAGCATAACATAAAATATTTTCATATTTGCACAAAAAATTTGAATAAAGG 101043
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                                                                                                                                                                                                                                                         NOTE: This is a PHASE2 sequence. Gaps are shown by nnnnn. Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      903 GTCTTATTAAAAAAAATTATGTATCTATTATTATTTATTATGACTTGATTCGTCATCA 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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1 88356: contig of 88356 bp in length
     HINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 113825,
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88557 113825: Contig of 25269 bp in length.
Location/Qualiflers
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82.0%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="OSJNBb0020011"
/clone_lib="CUGI-OSJNBb"
25501 c 25985 g 30469 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                         Web site: http://www.ncgr.ac.cn
----- Summary Statistics
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/organism="Oryza sativa"
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/db_xref="taxon:4530"
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                                                                                                                                                                                                 Assembly program: phrap
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                                      bhan@ncgr.ac.cn
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                                                                                                                     /rpt_family="Ar_rich"
/rpt_family="Ar_rich"
/rpt_family="Ar_rich"
complement(5251..55381)
/rpt_family="Ar_rich"
/rpt_family="Oryza sativa gene, repeat sequence Micropon-3
gil4586621[dbj|AB010113.1|AB010113"
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gil4586620[dbj|AB010113.1|AB010113"
/rpt_family="Cryza sativa gene, repeat sequence Micropon-4
gil4586620[dbj|AB010112.1|AB010112"
                                                                                                                                                                                                                                                                                                                                                                                             complement(56244. .56319)
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gi|4586662|db||AB010113.1|AB010113"
complement(56244. .56317)
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gi|4586620|db||AB010112.1|AB010112"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-JUN-2002) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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86.8%; Pred. No. 1.5e-22;
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                                                 /rpt_family="(TAA)n"
.49781)
                             /rpt_family="AT_rich" complement(50582. .500
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Oryza sativa
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KEYWORDS

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COMMENT

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Submitted (21-DEC-2001) Indian Initiative for Rice Genome Submitted (21-DEC-2001) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India Research Program; Rennondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan Rosearch Program; Rannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan * NOTE: This is a 'working draft' sequence. It currently * consists of 5 conligs. Gaps between the contigs * are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have * provided by the submitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 21-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrbartoideae; Orgyzae Oryzae. 1 (bases 1 to 158805) Mohanty, A., *Sasaki, T., *Matsumoto, T., *Yamamoto, K., Bharti, A.K., Rayhuvanshi, S., Khurana, P., Khurana, J.P. and Tyagi, A.K. Oryza sativa chromosome 11 PAC clone P0480H08, sequencing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uppublished

( bases 1 to 158805)

Mohanty,A., #Sasaki,T., #Matsumoto,T., #Yamamoto,K., Bharti,A.K., Raghuvanshi,S., Khurana,P., Khurana,J.P. and Tyagi,A.K. Direct Submission
90343 GATTCATCAAATGTTCTTTAAGCATGACATAAATATTTTTCATATTTTGCACAAAATTT 90402
                                                                                                                                                                                                                                        90403 TTAAATAACGAATGGTTAAAGGTTAGTCGAAAAGTCAATGGCGTCATACATTAAAATA 90462
                                                                951 GATTCGTCATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAAA----- 1005
                                                                                                                                                                                                        1006 --AAAAAAAGGAAFGGTCAAATGTTAGTCGAAAAGTCAATGGTGTATATAAATA 1063
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1 94637 94636 contig of 94636 bp in length 94637 136689; contig of 41935 bp in length 13690 136789; gap of unknown length 136790 140339; contig of 5550 bp in length 136790 140339; gap of unknown length 140390 140339; gap of unknown length
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/cultivar="Nipponbare"
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/db_xref="taxon:4530"
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Bedical Center Dr. Rockville, MD 20850, USA
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Medical Center Dr. Rockville, MD 20850, USA

* NOTE: This sequence version replaced gi:18767489.

* NOTE: This Sequence The Contigs.
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 10516 10615 contig of 10355 bp in length
* 23448 23771: contig of 10355 bp in length
* 36772 36871: gap of unknown length
* 36772 36871: gap of unknown length
* 44540 44640 44639; gap of unknown length
* 44540 44640 44639; gap of unknown length
* 44540 44640 12641: contig of 28002 bp in length
                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Lo 164852) La (Loase 1 to 164852) Lul (Loase 
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Submitted (19-JUM-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
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Best Local Similarity 86.6%; Pred. No. 5e-22;
Matches 220; Conservative 0; Mismatches 27; Indels
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/db_xref="taxon:4530"
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Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
The nucleotide sequence of this BAC clone was generated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO7YPX
Oryza sativa chromosome 12 clone OJ1618_C05, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
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Dikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 169663)
Cholsne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Segurens, B., Orjeda, G., Scarpelli, C., Salanoubat, M., Welssenbach, J. and Quetier, E., Scarpelli, C., Salanoubat, M., Oryza, Sativa chromosome 12 sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submission Submission Submitted (26-JUL-2002) Genoscope - Centre National de Sequencage : BP 191 91006 EVPY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr. - Web : www.genoscope.cns.fr) On Jul 29, 2002 this sequence version replaced gi:19715885. IMPORTANT: This sequence is unfinished and does not necessarly
                                                                                                                                                                                                                                                                                                                        D 132432 AAATTICGAATAAAAGAATAGTCAAACGTIGGTCGAAAAGTCAACGGCATCATACATTA 132491
                                                                                                 Db 132252 ATGTTAGTTTTAACTAATACTACCTCCATATTTTAATGTGCAACGCCGTTTACTTTTGT 132311
                                                                                                                                                              DD 132372 GACTIGATICGECCATCAARGETCTTTAAGCAFGACATAAATAFTTTCATATTTGCACAA 132431
                                                                                                                                                                                                                      946 GACTICALTCGICALCAAATALTITITIAAGCAIGACATAAACAITTICALAITTIGCAAAA 1005
                                                                                                                                                                                                                                                                                                 1006 A-----AAAAAAAGGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTA 1058
                                                                                                                                       ATGGACCTATTACTTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGT 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequencing data.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                        Indels
    5.9e-22;
ches 31;
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46256 a 37378 c 36384 g 49645 t
  Pred. No. 5.9e
0; Mismatches
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/sub_species="japonica"
/db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                     Db 132492 AAATACGGAGGAGTACTTG 132511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="12
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AL713952.2 GI:22003292
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    85.4%;
                      Conservative
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Best Local Similarity
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                      222;
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                    Matches
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CNS07YPX
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PAT 21-JUN-2002
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Plant genes that confer resistance to strains of magnaporthe grisea
having avrl co39 cultivar specificity gene
Patent: WO 0234927.A 5 02-MAY-2003;
WISCONSIN ALUMNI RES FOUND (US); The Secretary of Agriculture (US)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
33891 TAGATGAGATCACCGAAATATTTCATAACAACCAATTAAGTTGCTTCATACATGTACTGT 33832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33831 GGAGATCGCCTTGGTACTCCAATACTCCCTCTGTATTTTAATGTATGACGTTGTTGACTTT 33772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                942 TIATGACTIGATICGICAICAAATATTTTTAAGCAIGACATAAACATTTTCATATTTGC 1001
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Local Similarity 76.2%; Pred. No. 7.3e-22;
Hes 244; Conservative 0; Mismatch.
                                                                                                                                                                                                                                                                                                                                                                                linear
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/db_xref="taxon:4530"
26676 a 19760 c 17854 g 27262 t
                                                                                                                                                                                                                                                                                                                                                                    Sequence 5 from Patent W00234927.
AX429455
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HTG 13-MAY-2002
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Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 154494)
Khurana, J.P., #Linton, B.W., #Messing, J., Mohanty, A., Bharti, A.K., Raghuwanshi, S., Khurana, P. and Tyagi, A.K.
Oryza sativa (japoica cultivar-group) chromosome 11 BAC clone
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Khurana, J.P., #Linton, E.W., #Messing, J., Mohanty, A., Bharti, A.K., Raghuvanshi, S., Khurana, P. and Tyagi, A.K.

Raghuvanshi, S., Khurana, P. and Tyagi, A.K.

Bubmitted (13-MAY-2002) Indian Initiative for Rice Genome Sequencing, Department of Plant Wolecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India # The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
# The Plant Genome Initiative at Rutgers - Waksman Institute,
Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * This sequence will be replaced

* Dy the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1206 conting of 1206 bp in length

1207 21093: conting of 1976 bp in length

21094 21193: conting of 1977 bp in length

21194 64937: conting of 43744 bp in length

64938 65037: gap of unknown length

65938 13212: conting of 18284 bp in length

81322 81421: gap of unknown length

81322 81421: gap of unknown length

113558 113577: conting of 1828 bp in length

11358 113957: conting of 0 unknown length

11358 113957: gap of unknown length

113958 113954: gap of unknown length
                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group) chromosome 11 clone
Ba0042,005, *** SEQUENCING IN PROGRESS ***, 7 ordered pieces.
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Location/Qualifiers
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/sub_species="japonica cultivar-group"
/db_xref="taxon:39947"
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Pred. No. 9.4e-22;
                                                                                                                                                                                                                             DNA
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                                                          Db 103483 GAGGGAGTATGTTTTTCAATGCATTA 103457
                                                                                                                                                                                                                             154494 bp
                             1066 GAGGGATTATATGGGATAGCTACAGTA 1092
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44561 a 32837 c 31980 q
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HTG; HTGS_PHASE2.
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (30-JAN-2002) Takuji Sasaki, National Institute of Submitted (30-JAN-2002) Takuji Sasaki, National Institute of Agrobiogical Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8802, Japan (E-mail:tsasaki@inas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, NGTE: 11-208-38-7441, Fax:81-208-38-7465)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                 AP004691 ltnear HTG 21-MAR-2002 Oryza sativa (japonica cultivar-group) chromosome 8 clone P0453D01, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza
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clone:P0453D01.
33651 ACAAAAATTTTGAATAAAACGAATGGTCAAATGTTGATCGAAAAGTCAACGCCGTCATAC 33592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          833 TATTACTTATTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGT 892
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
clone:P0453D01
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Pred. No. 8.6e-22;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Only in Database (2002)
2 (bases 1 to 148441)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
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42350 a 31475 c 33016 g 41500 t
                                                                                    /chromosome="8'
                                                    1055 ATTAAAATACGGAGGGATTA 1074
                                                                                                                                                                                                                                                                                                                                                             AP004691.1 GI:18447950
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Best Local Similarity 83.9%;
Matches 224; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2
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TITLE
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[E-mail:tsasaki@nias.aifrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7466)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group) chromosome 8 clone P0024c06, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Oryza.
                                                                                     DD 144949 GATGATAGGCAAGTGAAGCACGTGCTTTATTTTATTACTACCTCCGTATTTAATGCAT 145008
                                                                                                                                                                                                           Db 145009 GACGTCGTTGACTTTTTGTCTAATGTTTTGACCÄTTCGTCTTATTCAAAAAATTTATGTAA 145068
                                                                                                                                                                                                                                                                                                               Db 145069 TTATCATTTATTATTATGACTTGATTTGTTATCAAATGTTCTTTAAGCATGACATAAA 145128
                                                                                                                                                                                                                                                                                                                                                                                                    DD 145129 TATTICATATITGCACAAAATTITIGAATAAAACGAAIGGTCAAACAIIGGTCGAAAAG 145188
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Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0024C06.
                                                       807 GTTGCAACGGAATAGTAATATGGACCTATTACTTACTACTACTACTACTATTTTAATGTAT 866
                                                                                                                                                          GACGCCGTTCACTTTTTGTCCAACGTTTGACCATTCGTCTTATTAAAAAAATTATGTAT 926
     Gaps
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Direct Submission
Submitted (29-MAY-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
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                                                                                                                                                                                                                                                             CTATTATTTATTTATTATGACTTGATTCGTCATCAAATATTTTTAAGCATGACATAAA
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1 22904: contig of 2294 bp in length
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23082 23186: gap of 105 bp
23187 179486: contig of 156300 bp in length.
Location/Qualifiers
     Indels
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23081 23081: contig of 1 bp in length
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  0; Mismatches
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2 (bases 1 to 179486)
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                                                                                                                                                                                                                                                                                                                           1010 ---AAAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGG 1066
                                                                                                                                                                                                                         834 ATTACITATIACICICCATAITITAAFGTATGGACGCCGTTCACTTFFFGTCCAACGTT 893
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                                                                               589 others
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                                                                                                                                     Score 184.6; DB 2;
Pred. No. 1.2e-21;
0; Mismatches 29;
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                                                                               50872 a 39291 c 39711 g 49023
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
/clone="P0024C06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: March 26, 2003, 14:00:53 Job time: 7637.65 secs
                                                                                                                                       Query Match 8.4%;
Best Local Similarity 85.9%;
Matches 219; Conservative
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993_DAT:*
                                                                                                                                                                                                                                                March 25, 2003, 18:27:39; Search time 335.492 Seconds
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
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Result	11t		Query				
z	No.	Score	Match	re Match Length DB I	8	QI.	Description
•					:		
υ	7	185.6	8.4	91552	24	AAD38803	BAC clone K6P36 fr
	(7)	125.2	5.7	807	21	AAC52171	Arabidopsis thalia
O	m	124.4	5.7	356	24	ABQ85736	Arabidopsis thalia
	4	124.4	5.7	1126	21	AAC47067	Arabidopsis thalia
	ហ	111.2	5.1	4569	24	ABK15663	Rice lipoxydenase
	9	110.2	5.0	689	24	ABQ65731	Arabidopsis thalia
	_	106.6	4.8	5241	23	AAA99467	Sakuranetin syntha
	æ	101	4.6	7175	13	AAV35027	Oryza sativa MLO q
υ	6	100	4.5	33675	24	AAD31202	Oryza sativa qcpE

BAC clone E2P5 fro Rice lipoxygenase BAC clone K6P36 fr Arabidopsis thalia Arabidopsis thalia Oryza sativa patho Rice sucrose phosp Arabidopsis thalia Rice beta-glucanas Sakuranetin syntha		MENTS 39. tivar; CO39; avirulence gene; sgenic plant; plant breeding; ral; plant protectant; ds. Durfee TJ;
ADD38804 ABK15663 AAD38803 AAC48763 AAC44265 AAC73703 AAC4276 AAC4276 AAC4276 AAC4276	AAX32297 AAX32297 AAX32297 AAX32297 AAX32597 AAA32466 AAA9466 AAA938802 AAC17703 AAC19703 AAC19703 AAC19703 AAC19703 AAC19762 AAC1762	ALIGN ALIGN Tice cul in; tran ticultu ticultu EFOUND. E.
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69300 4569 91552 694 1695 1031 2317 5241	1978 33675 33675 1978 1978 1978 1979 1979 1979 1979 1979	DNA; t ent t ent 1; In ast p litura O-US4 S:-242 S:-242 ML, ML,
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0 8 8 4 9 1 1 1 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	22222222222222222222222222222222222222	AD38803 s AAD38803; 23-SEP-200 BAC clone Rice; chro AVR1-C039; resistance Oryza sati WO20023492 02-MAY-200 09-UUL-200 09-UUL-200 09-UUL-200 WISC) WI (USDA) US Lieong SA, WPI; 2002-
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990S-0138847.
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99US-0136021.
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99US-0135353.
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99US-0140695.
99US-0140823.
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99US-0142390.
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   25-FEB-2000; 2000EP-0301439
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99US-01375
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07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
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16 - 70N - 1999)
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                                                        23-MAR-1999,
25-MAR-1999,
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01-APR-1999,
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16-APR-1999,
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23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
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21-JUN-1999;
22-JUN-1999;
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28-JUN-1999;
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06-MAY-1
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14-MAY-1
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21-MAY-1
24-MAY-1
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27-MAY-1
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01-JUN-1
03-JUN-1
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19-MAY-1
                                                                                                                                                                                                                                                                                                                         14-MAY-
   The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and 861094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-CO39. The Pi-CO39(T) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen. Magnaporthe grisea and other pathogens. The pi-CO39(T) nucleic acids may be used as probes to detect the presence of pure Pi-CO39(T) proteins. Purified gene products of Pi-CO39(T) are useful in producing polyclonal or monoclonal artibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(t) are useful for plant breading or directly in agricultural or horitualtural applications. The present sequence is BAC clone K6936 from rice variety CO39.
                                                                                                                                                                                                                                                                                                                                                                                          33772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33891 TAGATGAGATCACCCAAATATTTCATAACAACCAATTAAGTTGCTTCATACATGTACTGT 33832
                                                                                                                                                                                                                                                                                                                                                                                                                         942 ITATGACTTGATTCGTCATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTGC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1002 AAAAA-----AAAAAAAAGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATAC 1054
New PiCO39(t) polynucleotides from chromosome 11 of indica rice cultivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39
                                                                                                                                                                                                                                                                                                                                                                                                                 941
                                                                                                                                                                                                                                                                                                                      762 TATACTAGAGAGTTAAAAATTATTACAAAACTAACTGTATACCCGTTGCAACGGAATAG 821
                                                                                                                                                                                                                                                                                                7; Gaps
                                                                                                                                                                                                                                                                                                                                                                   822 TAATATGGACCTATTACTTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTT
                                                                                                                                                                                                                                                                                                                                                                               TIGICCAACGITIGACCALTCGTCTLALTAAAAAATTATGTATCTATTATTTTA
                                                                                                                                                                                                                                                                       Query Match 8.4%; Score 185.6; DB 24; Length 91552; Best Local Similarity 76.2%; Pred. No. 7.5e-30;
                                                                                                                                                                                                                                                    Sequence 91552 BP; 26676 A; 19760 C; 17854 G; 27262 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 70520
                                                                                                                                                                                                                                                                                                0; Mismatches
                                                       Example 2; Page 68-110; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33591 GTTAAATACGGAGGAGTA 33572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1055 ATTAAAATACGGAGGATTA 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC52171 standard; DNA; 807 BP
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990S-0148319.
990S-0148341.
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990S-0149684.
990S-0149136.
990S-0149426.
990S-0149929.
990S-0149929.
990S-0149929.
990S-015066.
990S-015066.
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990S-01444335,
990S-0144632,
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990S-0144614,
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99US-0155139.
99US-0155486.
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99US-0142920,
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30-AUG-1999;
31-AUG-1999;
09-70L-1999;
12-70L-1999;
13-70L-1999;
14-70L-1999;
15-70L-1999;
16-70L-1999;
19-70L-1999;
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20-70L-1999;
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22-JUL-1999;
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26 - JUL - 1999;
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27 - JUL - 1999;
28 - JUL - 1999;
02 - AUG - 1999;
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03 - AUG - 1999;
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21-JUL-1999;
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21-JUL-1999;
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04-AUG-1999;
05-AUG-1999;
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24-SEP-1999;
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25-AUG-1999;
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07-SEP-1999;
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09-AUG-1999
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1334 AAGATTTGCAGGTGCGAGATCACTCTTCACCAAGCGCCACGGCGTCATCCGCGCCGAG 1393
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                                                                                                                                                                                                                                                                                                                                                                                                   1214 GAGAAGGIGAAGGAGCACAICGAGGAGAAGGCGGGGAGAGCAGIGGCGAAGCACAGCCAG 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                         1274 CTTGTGAAGGAGGTGGACGTGCGCCTCTCCGCCGCGCGGGGCGAGCTCAGCCGAGGTCCC 1333
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 125.2; DB 21; Length 807;
65.9%; Pred. No. 1.5e-17;
Live 2; Mismatches 90; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana expressed polynucleotide SEQ ID NO 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1454 CTCAGGAAGATCAAGGAGAAGGAGACCGAC 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S-0156458.
990S-0156596.
990S-0157753.
990S-0157765.
990S-0158029.
990S-0158029.
990S-0159294.
990S-0159330.
990S-0159331.
990S-0159331.
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990S-0160814-
990S-0160815-
990S-0160981-
990S-0160981-
990S-0161405-
990S-0161405-
990S-0161359-
990S-0161359-
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990S-0161359-
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990S-0161359-
990S-0161359-
990S-0161353-
990S-0161933-
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ID ABQ85736 standard; DNA; 356
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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nes 178; Conserv
28-SEP-1999;
29-SEP-1999;
05-CCT-1999;
06-CCT-1999;
06-CCT-1999;
08-CCT-1999;
13-CCT-1999;
13-CCT-1999;
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14-CCT-1999;
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22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
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26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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28-0CT-1999;
28-0CT-1999;
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Matches
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Plant; Arabidopsis; transgenic; fungicide; insecticide; ds.

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23-MAY-2002

(HAMI/) (PRIC/)

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1394 GAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGCCTCCTCCATCATCAAGAGGAAG 1453
                 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                           metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                            Arabidopsis thaliana DNA fragment SEQ ID NO: 52441.
                                                              1454 CICAGGAAGAICAAGGAGAAGGAGACCGAC 1483
                                                                              44 CTGAGGAAGATCAAGGAGAAGGACTCAGAC 15
                                                                                                                                                                    AAC47067 standard; DNA; 1126 BP.
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990S-0132048.
990S-0132407.
990S-0132484.
990S-0132485.
990S-0132487.
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990S-0134218.
990S-0134219.
990S-013421.
990S-0134370.
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99US-0136782.
99US-0137222.
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990S-0137502.
990S-0137724.
990S-0138094.
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99US-0130449.
99US-0130510.
99US-0130891.
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99US-0135629.
99US-0136021.
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99US-0123548.
99US-0125788.
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99US-0126785.
99US-0127462.
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99US-0128714.
99US-0129845.
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                                                                                                                                                                                                                             18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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20-MAY-1999;
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27-MAY-1999;
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08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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09-MAR-1999;
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14-may-1999;
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30-APR-1
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23-APR-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1214 GAGAAGGTGAAGGAGCACATCGAGGAGGAGGGGGGGAGGAGCAGTGGCGAAGCACAGCCAG 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1334 AAGATTTGCAGGTGCGAGATCACTCTTTCACCAAGCGCCACGGCGTCATCCGCGCCGAG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 AGGATTCGAACATGTGAGGTGACATTGTTTACAAAGAAGCATGGTGTTTGCTGAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences of Arabidopsis thaliana and their encoded products are useful to produce transgenic plants, to screen for biologically active agents such as fungicides and insecticides and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 GAGCCAATTAAGCAGCATGTTGAAGAGAAAGTAGGCAAATCTGTTCAGAAACACAGTCAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 CTTGTGAGAGAAGTTGATGTAAGACTCTCTGTTCGTGGTGGAGAGTTTGGTAAAGGCCCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Price JL, Raines TM, Yu Y;
Ledford BL, Woessner JP, Haas WD;
Davis KR, Allen K, Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 124.4; DB 24; Length 356; 66.3%; Pred. No. 1.6e-17; ative 0; Mismatches 91; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 606; 18pp + Sequence Listing; English.
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A, Mathew AV, Le
r M, Slater T, I
                                                                                         26-JAN-2001; 2001US-0770791.
                                                                                                                        27-JAN-2000; 2000US-178480P.
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Page A, Ma
Kricker M,
                                                                                                                                                                      AN Y.
HAMILTON C M.
PRICE J L.
RAINES T M.
                                                                                                                                                                                                                                                              PAGE A.
MATHEW A V.
LEDFORD B L.
WOESSNER J P.
   Arabidopsis thaliana.
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GARCIA C A.
KRICKER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-479265/51.
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DAVIS K R.
ALLEN K.
HOFFMAN N.
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                                                                                                                                                       GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic studies
                                US2002062014-A1.
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Gorlach J, Rameaka JG,

(KRIC/) (SLAT/) (DAVI/) (ALLE/) (HOFF/)

(HAAS/) (GARC/)

WOES/)

Garcia CA, Hurban P;

Query Match

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990S-0139453.
990S-0139492.
990S-0139454.
990S-0139455.
                                                                                               990S-0139763
990S-0139763
990S-0139817
990S-0140353
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990S-0140695
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990S-0141842
990S-0141842
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99US-0142977.
99US-0143542.
99US-0143624.
99US-0144005.
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99US-0139457.
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99US-0139459.
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990S-014576.
990S-0145918.
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990S-0145951.
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990S-0147204.
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990S-0147192.
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99US-0147303.
99US-0147416.
99US-0147493.
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990S-0145086
990S-0145088
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99US-0144331
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99US-0146389
10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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05-AUG-1999;
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PR 10-ANG-1999; 990g-0148171.
PR 11-ANG-1999; 990g-0148319.
PR 13-ANG-1999; 990g-0148311.
PR 13-ANG-1999; 990g-0148319.
PR 13-ANG-1999; 990g-014936.
PR 13-ANG-1999; 990g-0149426.
PR 20-ANG-1999; 990g-0149426.
PR 20-ANG-1999; 990g-0149426.
PR 20-ANG-1999; 990g-0149426.
PR 20-ANG-1999; 990g-0149929.
PR 20-ANG-1999; 990g-0149920.
PR 20-ANG-1999; 990g-0151066.
PR 20-ANG-1999; 990g-015209.
PR 20-ANG-1999; 990g-015209.
PR 20-ANG-1999; 990g-015209.
PR 20-ANG-1999; 990g-015909.
PR 20-ANG-1999; 9

Ouery Match 5.7%; Score 124.4; DB 21; Length 1126; Best Local Similarity 66.3%; Pred. No. 2.6e-17; Matches 179; Conservative 0; Mismatches 91; Indels 0; Gaps

1214 GAGAAGGTGAAGGAGCACATCGAGGAGAAGGCGGGGAGAGCAGTGGCGAAGCACAGCCAG 1273

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GORLACH J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ65731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MATH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inducible expression of an associated nucleotide sequence. Also included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the lipoxygenase grene, promoter fragments, the lipoxygenase transit peptide which directs expressed proteins to the plastid, a vector comprising the promoter or fragments and a transgenic plant comprising the vector. The promoter or fragments are useful for expressing a nucleotide sequence of interest. The transit peptide is useful for targeting an associated protein of interest to plastids. A nucleic acid which expresses polypeptide having lipoxygenase activity is useful for inhibiting fungal mycotoxins when transformed into a plant. The lipoxygenase is useful for inhibiting fungal mycotoxins when transformed into a plant. The useful for regulating transcription of a chemically inducible but not wound or pathogen inducible gene, which involves applying a chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (a promoter rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase) capable of driving chemically-inducible but not wound or pathogen-
                                                                         1393
                                                                                                                         1453
                         1274 CTTGTGAAGGAGGTGGACGTGCGCCTCTCCGCCCGCGCGTGGCGAGCTCAGCCCGAGGTCCC 1333
                                                                                                                                         381 GAGCCAATTAAGCAGCATGTTGAAGAGAAAGTAGGCAAATCTGTTCAGAAACACAGTCAT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound or pathogen-inducible expression of an associated nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                Rice; ds; lipoxygenase; RCI-1; transgenic; plant; plant antifungal; rice chemically induced cDNA; promoter; transit peptide; plastid; fungal mycotoxin inhibitor; plant breeding; pBSK+LOX4a.
                                      1394 GAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGCCTCCTCCATCAAGAGGAAG
                                                                                                                                                                          1454 CTCAGGAAGATCAAGGAGAAGGAGACCGAC 1483
                                                                                                                                                                                                 621 CTGAGGAAGATCAAGGAGAAGGACTCAGAC 650
                                                                                                                                                                                                                                                                                                                                        Rice lipoxygenase gene 4.5kb fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawton KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 68-69; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                               ABK15663 standard; DNA; 4569 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2001; 2001WO-EP08085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-2000; 2000GB-0017275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-0022739
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                                                                                                                                                                                                                                                                                        ABK15663;
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ABK15663
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regulator to a plant or seed containing a chemically regulatable nucleotide sequence. Transgenic plants as described above are useful for breeding improved plant lines that for example increases the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties. New crops with improved stress tolerance can be obtained that, due to their petinised genetic equipment yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions. The present sequence is the 4.5kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana, thale cress, plant; transgenic; GMO; disease; stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide; insecticide; antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2963 AIAGFACTITAAGFGFGATTTAFATTTTTACATTTACATAAAATTTTTGAATAAGACGA 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2845 IACTACCICTGTTTTTTAATAGACGCCGTTGACTTTTTTCTCACATGTTTGACCATTC 2904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963 AATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAAAA-----AAAAAAAGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3023 ATGGTCAAACATGGGAGAAAAGTCAACGGCGTCATCTATTAAAAACGGAGAGAGTATA 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      843 IACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCATTC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  903 GICTTATTAAAAAAAATTATGTATCTATTATTTATTATTATTATGACTTGATTCGTCATCA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 111.2; DB 24; Length 4569;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 4569 BP; 1234 A; 1051 C; 980 G; 1304 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78; Indels
                                                                                                                                                                                                                                                                                                  fragment of the RCI-1 gene from plasmid pBSK+LOX4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana polynucleotide SEQ ID NO 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3083 TGATTCATCGGAATTAAAAAATAGACGGTATA 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      5.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 68.4
Matches 186; Conservative
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HAMILTON C M.
PRICE J L.
RAINES T M.
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MATHEW A V.
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RAMEAKA J G.
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Barley; MLO; mildew; pathogen; resistance; ss.
    transgenic plant;
                                                                                                                                                                                          WPI; 2000-572186/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 183; Conserv
                                                                                                                                                                                                     P-PSDB; AAB26843.
    antibacterial;
                                                 WO200052174-A1
                                                                                                                                             (NISC-) JAPAN
                            Oryza sativa
                                                                                                                      04-MAR-1999;
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                                                                        08-SEP-2000
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                                                                                                                                                                    Kodama 0;
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Matches
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    δλ
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XBXAXXAXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                           The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ65424-ABQ66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics).
                                                                                                                                                                                                                                                                                                                                                                   printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1214 GAGAAGGTGAAGGAGCACATCGAGGAGAAGGCGGGAGAGCAGTGGCGAAGCACAGCCAG 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1274 CTTGTGAAGGAGGTGGACGTGCGCCTCTCCGCCCGCGGTGGCGAGCTCAGCCGAGGTCCC 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1334 AAGATTTGCAGGTGCGAGATCACTCTTTCACCAAGCGCCACGGCGTCATCCGCGCCGAG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1394 GAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGCCTCCTCCATCATCAAGAGGAAG 1453
                                                                                                                                                                                   New nucleic acid that hybridizes to Arabidopsis thaliana sequences, useful e.g. for preparing transgenic plants with increased resistance or altered metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 GAGCCAATTAAGCAGCATGTTGAAGAGAAAGTAGGCAAATCTGTTCAGAAACACAGTCAT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ø);
                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the pr specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=999909770149.
                                                                                                          Yu Y;
JP, Haas W
Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sakuranetin synthetase; naringenin 7-0-methyltransferase; NOMT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                     5.0%; Score 110.2; DB 24; Length 689; 62.2%; Pred. No. 2.7e-14;
Live 0; Mismatches 99; Indels 0;
                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 308; 40pp + Sequence Listing; English.
                                                                                                                      Woessner
Allen K,
                                                                                                           Raines IM,
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 689 BP; 192 A; 136 C; 174 G; 176 T; 11 other;
                                                                                                          Price JL, Raj
Ledford BL,
, Davis KR, 7
                                                                                                         Hamilton CM, Pr.
A, Mathew AV, La
r M, Slater T, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1454 CTCAGGAAGATCAAGGAGAAGG 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5241 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakuranetin synthase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA99467 standard; DNA;
                                                                                                                     Page A, N
Kricker M,
HAAS W D.
GARCIA C A.
KRICKER M.
                                                                                                                                                                  WPI; 2002-479224/51.
                                     SLATER T.
DAVIS K R.
ALLEN K. '
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                          An Y,
                                                                                    HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-2001
                                                                                                                     Rameaka JG,
                                                                                                                                Garcia CA,
Hurban P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              163;
                                                                                                           Gorlach J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA99467;
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                                                (DAVI/)
(ALLE/)
(HOFF/)
                                                                                    (HURB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                           (KRIC/)
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This invention relates to a sakuranetin synthetase gene encoding a protein with naringenin 7-0-methyltransferase (NOMT) sctivity and promoter activity. The invention includes a recombinant vector including the sakuranetin synthetase DNA and host cells transformed with the vector. The sakuranetin synthetase protein has antibacterial activity and is used to produce transpent plants with antibacterial characteristics. The present sequence represents the sakuranetin synthetase gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   960 TCAAATATTTTTAAGCATGACATAAACATTTTTCATATTTGCAAAA-----AAAAAAA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1013 ACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGAT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sakuranetin synthetase gene encoding protein with naringenin 7-0-methyltransferase activity in rice cells and promoter activity, used to derive sakuranetin from naringenin easily in plants to impart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            840 TATTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCA 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                900 TTCGICTTAAAAAAAATTAATGIATCIATTATTTATTTATTATTATGACTTGATTCGTCA 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5241 BP; 1542 A; 1138 C; 1094 G; 1467 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8%; Score 106.6; DB 21; 63.3%; Pred. No. 4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4e-13;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 43-46; 57pp; Japanese.
                                                                                                                                          SCI & TECHNOLOGY CORP
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03-MAR-2000; 2000WO-JP01306
                                                                        99JP-0057748
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*tag= c
note= "This region corresponds to rice GCPE protein #1"
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//tote="This region corresponds to rice GCPE protein #1"
//cons_splice= (5'site:YES, 3'site:NO)
6924..7019
                                                      "Rice GCPE protein #1"
                                                                                         "Rice GCPE protein #2"
                     location/Qualifiers
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0134..10293
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0694..10798
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6924..11129
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8515..8589
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8590..9011
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9072..9162
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9163..9225
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9226..9327
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9328..9472
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9473..9588
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9589..9730
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1731..9950
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8154..8252
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7270..7343
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7814..7922
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7923..8153
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7344..7444
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7445..7524
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8370..8514
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                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcpE gene; methyl-D-erythritol phosphate; MEP; dimethylallyl diphosphate; transgenic plant; isoprenoid compound; tcoophero; isopentyl alphosphate; food; feed source; transfection; single nucleotide polymorphism; SNP; exidative stress tolerance; UV tolerance; transformation; rice; plant;
                                                                                                                                                                                                                                                                                    The sequence is that of the MLO gene, wild-type MLO exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or our cour-competition of MLO function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also he used for identifying compounds able to stimulate a defence response in a plant by interaction with encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1971 ATTYAAAAAATTYAAAGTAATTATTAATTCTTTTTCTACCATTGGATTCCTAAATAT 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       968 ITITIAAGCATGACATAAACATTITCATATTIGCAAAA------AAAAAAAAAAGG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908 ATTAAAAAATTATGTATCTATTATTTATTATTATGACTTGATTCGTCATCAAATAT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                848 CCTCCATATTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCATTCGTCTT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021 TCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATAT 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated MIo gene of barley - used to develop products for the production of transgenic plants which have increased pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 101; DB 19; Length 7175; 67.5%; Pred. No. 7.8e-12;
tive 0; Mismatches 70; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7175 BP; 2089 A; 1455 C; 1431 G; 2200 T; 0 other;
                                                                                                                                                                        Bueschges R, Panstruga R, Schulzelefert PMJ;
                                                                                                                                                  CENT INNOVATIONS LTD JOHN.
                                                                                                                                                                                                                                                                  Disclosure; Fig 8; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD31202 standard; DNA; 33675 BP.
                                                                                                    97GB-0004789.
96GB-0015879.
96GB-0022626.
                                                                              97WO-GB02046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa gcpE gene.
                                                                                                                                                                                               WPI; 1998-159149/14.
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                  (INNE-) INNES
                                                                                                    07-MAR-1997;
29-JUL-1996;
30-OCT-1996;
             Oryza sativa
                                                                                29-JUL-1997;
                                   WO9804586-A2
                                                          05-FEB-1998
                                                                                                                                                                                                                                              resistance
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AAD38804 standard; DNA; 69300 BP.

AAD38804/c

RESULT 10

AAD38804;

16578 ATCCTGTATCTATCGT 16563

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16698 AATATACTTTTATGTATACATATAGTTTTATATTTTCACAAAATTTTTGAATAAGATG 16639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gopE nucleic acid which is an essential gene of the methyl-D-erythritol phosphate pathway, encoding a fully defined GCPE protein which is useful for increasing levels of tocopherol substrates in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16757 GICTTATICAAAAATTITAAATAAATAATTATTI-ITITCCIAICATTGATICATTGITA 16699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rohmer M,
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/*tag= ag
10799..11027
/*tag= ah
11028..11129
/*tag= ai
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Venkatesh TV,
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P-PSDB; AAE19651, AAE19652.
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ses 173; Conserv
                                                                                                                                                                                                                               WO200212478-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boronat A, Ca
                                                                                                                                                                                                                                                                                                           14-FEB-2002
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The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-CO39. The P1-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The P1-CO39(t) nucleic acids may be used as probes to detect the presence of p1-CO39(t) nucleic acids may be used as probes to detect the presence of pure P1-CO39(t) proteins. Purified gene products of P1-CO39(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of P1-CO39(t) polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or hortcultural applications. The present sequence is BAC clone E2P5 from rice variety CO39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PiCO39(t) polynucleotides from chromosome 11 of Indica rice utilivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTAAAAAAATTATGTATCTATTATTTATTTATGACTTGATTCGTCATCAAATAT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCICCAIAITITAAIGIAIGACGCCGIICACTIIITGICCAACGIIIGACCAIICGICII 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69300 BP; 19720 A; 15094 C; 15006 G; 19380 T; 100 other;
                                                                                                                                          Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene; AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding; resistance; agricultural; horticultural; plant protectant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100; DB 24;
Pred. No. 3.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Durfee TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 110-142; 175pp; English.
                                                                                                        3AC clone E2P5 from rice variety CO39.
                                                                                                                                                                                                                                                                                                                                                                                                                             (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chauhan RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DEPT OF AGRICULTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.5%;
Best Local Similarity 67.4%;
                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-2001; 2001US-303897P.
                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000; 2000US-242313P
                                                                                                                                                                                                                                                                                                                                    19-0CT-2001; 2001WO-US46331
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leong SA, Farman ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-471442/50.
                                                                                                                                                                                                                                                             WO200234927-A2.
                                                                       23-SEP-2002
                                                                                                                                                                                                                         Oryza sativa.
                                                                                                                                                                                                                                                                                                02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USDA)
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Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΣ
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δ g QΥ g ď qq δŽ Length 4569;

DB 24;

Query Match

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Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound or pathogen-inducible expression of an associated nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice, ds, lipoxygenase; RCI-1; transgenic; plant; plant antifungal; rice chemically induced cDNA; promoter; transit peptide; plastid; fungal mycotoxin inhibitor; plant breeding; pBSK+LOX4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase) capable of driving chemically-inducible but not wound- or pathogen-
                                                                                                 1021 TCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice lipoxygenase gene 4.5kb fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG. (UYZU-) UNIV ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawton KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 68-69; 88pp; English.
                                                                                                                                                                                                                                                                               ABK15663 standard; DNA; 4569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2001; 2001WO-EP08085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-2000; 2000GB-0017275
15-SEP-2000; 2000GB-0022739
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-2002
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                                                                                                                                                                                                                                                                                                                                             ABK15663;
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XX AAC
XX ABK11
XX ABK11
XX ABK11
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XX ABK11
XX ABK12
XX ABK13
XX ABC2
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XX ABC2
XX ABC2
XX ABC2
XX ABC3
XX AB
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inducible expression of an ascolated nucleotide sequence. Also included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the lipoxygenase gene, promoter fragments, the lipoxygenase transit peptide which directs expressed proteins to the plastid, a vector comprising the promoter or fragments and a transgenic plant comprising the vector. The promoter or fragments are useful for expressing a nucleotide sequence of interest. The transit peptide is useful for targeting an associated protein of interest to plastids. A nucleic acid which expresses polypeptide having lipoxygenase activity is useful for inhibiting fungal mycotoxins when transformed into a plant. The lipoxygenase is useful for inhibiting fungal mycotoxins when transformed into a plant or the promoter is useful for regulating transcription of a chemically inducible but not cound or pathogen inducible gene, which involves applying a chemical crowled sequence. Transgenic plants as described above are useful for breading improved plant lines that for example increase the effectiveness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties.
invention relates to an isolated nucleic acid molecule (a promoter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality than products that were not able to tolerate comparable adverse developmental conditions. The present sequence is the 4.5\mathrm{kb}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New crops with improved stress tolerance can be obtained that, due their optimised genetic equipment yield harvested product of better
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment of the RCI-1 gene from plasmid pBSK+LOX4a.
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Sequence 4569 BP; 1234 A; 1051 C; 980 G; 1304 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one or more genes that confer resistance to strains of Magnaporthe grisse having avirulence gene AVRI-CO39. The Pi-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen. Magnaporthe grisse and other pathogens. The Pi-CO39(t) nucleic acids may be used as probes to detect the presence of and/or expression of Pi-CO39(t) genes, and to produce large quantities of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising
                                                                                                                                                                                                                                                                                            1078
                                                                                                                                                                                                                                                                                                                  2900 GGTCAAACAIGTGAGAAAAAGTCAACGGCGTCATTTAAAAAACAGAGGTAGTATTATTC 2841
                                                                                                           3021
                                                                                                                                               962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants
                                      Gaps
                                                                                                 3080 TACTCTCCGTTTTTTAATAGATGACGCCGTTGAĞTTTTCTCCCCATGTTTGACATTCT
                                                                        843 TACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCATTC
                                                                                                                                               903 GICTTATTAAAAAAAATTATGTATCTATTATTTATTTATTATGACTTGATTCGTCATCA
                                                                                                                                                                                   3020 GICTTATICAAAAITTTAIGTAAAIGIATAAGAIATAAAICACACTTAAAGTACTAIGA
                                                                                                                                                                                                                                                        2960 GIGATAAAACAATICATAACAAACTAAATTATAATTATAATTITITTAATAAAAGACGAAT
                                                                                                                                                                                                                                                                                            1019 GGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATATG
                                                                                                                                                                                                                        963 AATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAA----AAAAAAAAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice, chromosome 11; Indica rice cultivar; CO39; avirulence gene; AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding; resistance; agricultural; horticultural; plant protectant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar CO39 useful for conferring or improving resistance of to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39
                                      4
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                          2840 TTATATACAATCTAATCTACTAATGGTAAGCAAAAAATATTTT 2798
                                                                                                                                                                                                                                                                                                                                                                   1079 GGATAGCTACAGTAGCAGAGTCATGATAAAGTAGTAATGTGTT 1121
                                    0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Durfee TJ;
Score 98.6; DB 2
Pred. No. 2.1e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC clone K6P36 from rice variety C039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 68-110; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WISC ) WISCONSIN ALUMNI RES FOUND.
(USDA ) US DEPT OF AGRICULTURE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD38803 standard; DNA; 91552 BP
4.5%;
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09-JUL-2001; 2001US-303897P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-2002 (first entry)
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SA, Farman ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-471442/50.
                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-2001;
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                   Best Local Sim
Matches 175;
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AAD38803
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990S-0141842.
990S-0142154.
990S-0142365.
990S-0142393.
990S-014230.
990S-014297.
990S-0143542.
990S-0144005.
990S-0144005.
             990S-0132485.
990S-0132486.
990S-0132487.
990S-0132863.
990S-0134256.
990S-0134218.
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9905-0134219
9905-01344219
9905-01344219
9905-01346419
9905-0135124
9905-0135629
9905-0136320
9905-0136320
9905-0136320
9905-013724
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9905-0139455
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99US-0139461.
99US-0139462.
99US-0139463.
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990S-0139763
990S-0139897
990S-0140859
990S-0140354
990S-0140695
990S-0140991
990S-0141287
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990S-0144331.
990S-0144333.
990S-0144334.
990S-0144334.
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990S-0144884.
990S-0144814.
990S-0145086.
     99US-0132484
                                                                                        14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
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25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
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08-70N-1999)
10-70N-1999)
14-70N-1999)
16-70N-1999)
17-70N-1999)
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22-00N-1999;
23-00N-1999;
23-00N-1999;
24-00N-1999;
28-00N-1999;
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06-JUL-1999;
08-JUL-1999;
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14-JUL-1999;
15-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
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14-MAY-1999;
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18-JUN-1999;
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19-JUL-1999;
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20-JUL-1999;
                                                  11-MAY-1999;
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     pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(t) polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or hortkoultural applications. The present sequence is BAC clone K6P36 from rice variety CO39.
                                                                                                                                                                             33565 TAGTAAGTACTCCCTCCGTATTTTAACGTATGACGCCGTTGACTTTTCGATCAACATTTG 33624
                                                                                                                                                                                                                      1009 AAAAACGAATGGICAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAG 1058
                                                                                                                                                                                                        956 GICAICAAAIAITITITAAGCAIGACAIRAACAITITCAIAITIGCAAAAA-----AA 1008
                                                                                                                                                                   896 ACCAUTICGICITALIAAAAAAATTAIGTAICTAITATTITATTATTATTATGACTIGATIC 955
                                                                                                                             836 TACTIALTACTACCTCCATALTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTG 895
                                                                                                           7; Gaps
                                                                                       Query Match 4.5%; Score 98.2; DB 24; Length 91552; Best Local Similarity 65.6%; Pred. No. 9.8e-11; Matches 162; Conservative 0; Mismatches 78; Indels 7;
                                                                   Sequence 91552 BP; 26676 A; 19760 C; 17854 G; 27262 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 58679.
                                                                                                                                                                                                                                                                                                                                                       BP.
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99US-0123180.
99US-0123548.
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99US-0128714.
99US-0129845.
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99US-0126264.
99US-0126785.
99US-0127462.
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99US-0130891
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99US-0132048
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                     1069 GGATTAT 1075
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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05-MAR-1999;
09-MAR-1999;
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30-APR-1999;
30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1999;
08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2000
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19-APR-1999;
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1813 GGGAGATGAACGTCCTGTACAAGAGGAAGGAAGGCTTCGGTCTCATCGTCCCCAAGG 1872
                                                                                                                                                                                       1693 TGTGAATGCAGGTGGTGCGCACCAAGGTGTTCGAGATGCCGCCGCTGTCGGTGGAGGAGG 1752
                                                                                                                                                                                                                         1753 CGATGGAGCAGCTAGTGAATGTGGACCACAACTTCTACGCCTTCAGAGACGACGAGAAGACCG 1812
                                                                                                                                                                                                   282 CAGTCGAGCAGCTGGAACTAGTCAGTCAGCACTCTATGGCTTCCAAAATGAAGAAACTG 341
                                                                                                                                                                                                                                                                          342 GTGAGATAAACATAGTGTACAAGAGAAAAAGAAGGAGGTTACGGTCTGATAATCCCAAAGA 401
                                                                                                                                                                                                                                                                                                                                                                                                                         Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                     Ouery Match 4.3%; Score 95.4; DB 21; Length 694; Best Local Similarity 67.2%; Pred. No. 4.6e-11; Matches 135; Conservative 0; Mismatches 66; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ ID NO: 42224.
                                                                                                                                                                                                                                                                                           1873 GAGACGGTCATCTCCACAAGG 1893
                                                                                                                                                                                                                                                                                                            402 AAGACGGGAAGGCCGAGAAGG 422
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9905-012348.
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9905-0125788.
9905-012624.
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9905-0128234.
9905-0128714.
9905-0130077.
99US-0160768.
99US-0160710.
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99US-0160980.
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99US-0161404.
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99US-0161920.
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99US-0161993.
99US-0162142.
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                                                                            99US-0161406
99US-0161359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
21.0CT-1999;
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16-APR-1999;
19-APR-1999;
21-APR-1999;
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990S-0151303
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990S-015363
990S-0153758
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12-OCT-1999;
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15-SEP-1999;
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11-AUG-19
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990S-0144632. 990S-0144884. 990S-0144884. 990S-0145085. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145192. 990S-0145192. 990S-0145193. 990S-0145913. 990S-0145913. 990S-0145913. 990S-0147302. 990S-0147303. 990S-0149330. 990S-0149330. 990S-0149336. 990S-0149336. 990S-0149336. 990S-0149336. 990S-0149336. 990S-0149336. 990S-0149336. 990S-0149336. 990S-0149336.	990S-0153070. 990S-0154018 990S-0154039. 990S-0154039. 990S-0155139. 990S-0155486. 990S-0155659. 990S-0156596. 990S-0156596. 990S-0156596. 990S-0156596. 990S-015629. 990S-015823. 990S-015823. 990S-015823. 990S-015823.
20-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 24-JUL-1999; 27-JU	10.SEP 1999; 13.SEP 1999; 16.SEP 1999; 20.SEP 1999; 22.SEP 1999; 23.SEP 1999; 24.SEP 1999; 24.SEP 1999; 06.OCT 1999; 06.OCT 1999; 07.OCT 1999; 13.OCT 1999; 13.OCT 1999; 14.OCT 1999; 14.OCT 1999; 14.OCT 1999; 14.OCT 1999;
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0H08C466676686108144661666864407666646676678600466666	%11,544,00%,0,544,000,001,4%,4,0,4
9905-0130461 9905-0131449 9905-0132484 9905-0132487 9905-0132485 9905-0132485 9905-0132485 9905-0132485 9905-0132863 9905-0132863 9905-0132863 9905-0133263 9905-0133263 9905-0133219 9905-013322 9905-0133421 9905-0133621 9905-0133445 9905-0133455 9905-0133455 9905-0133455 9905-0133455 9905-0133455 9905-0133455 9905-0133455 9905-0133455 9905-0133456	990S-0140081 990S-0141091 990S-0141842 990S-0142154 990S-0142055 990S-0142059 990S-0142059 990S-0142970 990S-014394 990S-0144085 990S-0144085 990S-0144085 990S-0144085 990S-0144334 990S-0144334 990S-0144334
23-APR-1999; 28-APR-1999; 30-APR-1999; 30-APR-1999; 66-MAY-1999; 66-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 12-MAY-1999; 13-MAY-1999; 14-MAY-1999; 16-MAY-1999; 18-MAY-1999; 18-MA	28 - UNN - 1999; 29 - UNN - 1999; 30 - UNN - 1999; 01 - ULL - 1999; 02 - ULL - 1999; 06 - ULL - 1999; 06 - ULL - 1999; 07 - ULL - 1999; 12 - ULL - 1999; 13 - ULL - 1999; 14 - ULL - 1999; 15 - ULL - 1999; 16 - ULL - 1999; 17 - ULL - 1999; 18 - ULL - 1999; 19 - ULL - 1999;
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                                                                                                                                                                                                                                                              1693 IGTGAATGCAGGTGGTGCCACCAAGGTGTTCGAGATGCCGCCGCTGTCGGTGGAGGAGG 1752
                                                                                                                                                                                                                                                                                                    1753 CGAIGGAGCAGCIAGIGAAIGIGGACCACAACIICIACGCCIICAGAGACGAGAAGACCG 1812
                                                                                                                                                                                                                                                                                                                                           1813 GGGAGATGAACGTCCTGTACAAGAAGGAAGGAAGGAGGCTTCGGTCTCATCGTCCCCAAGG 1872
                                                                                                                                                                                                                                                                         240 TGATCAAGGAGATTGTCCGTACCAAGACTTTCGAGATGCCACCATTGACTGTCGCTGAGG 299
                                                                                                                                                                                                                                                                                                                360 GTGAGATAAACATAGTGTACAAGAGAAAAGAAGGAGGTTACGGTCTGATAATCCCAAAGA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pathogen inducible regulatory element; MAG-7; Magnaporthe grisea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa pathogen inducible regulatory element Pr-10c cDNA
                                                                                                                                                                                                                        Length 695;
                                                                                                                                                                                                                       4.3%; Score 95.4; DB 21;
67.2%; Pred. No. 4.6e-11;
tive 0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                1873 GAGACGGTCATCTCCACAAGG 1893
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99US-0161406.
99US-0161359.
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99US-0161992
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                                                                                     99US-0160980
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Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PURD ) PURDUE RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-0CT-1996;
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                                                                                                                                                                                 28-0CT-1999;
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                                              21-OCT-1999;
21-OCT-1999;
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                                                                 21-0CT-1999
                                                                                           22-0CT-19
22-0CT-19
25-0CT-11
25-0CT-11
25-0CT-11
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                                                                          21-0CT-1
22-0CT-1
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                                                                                                                                                                             The present sequence, Pr-10c, is a pathogen inducible regulatory element. It was identified by screening a Co39 rice seedling appeared in library with a cDNa clone, MAG-7 of a gene whose transcripts appeared in Co39 rice seedlings 72 hours after incoulation with Magnaporthe grisea. Induced expression of the Pr-10c gene was not detected after infection with M. grisea throughout a 144 hour time period. The Pr-10c sequence is used to make a novel plant expression vector comprising a pathogen-inducible regulatory element and a core promoter, where the regulatory element is selected from three rice genomic DNA sequences AMI93778-80. The vectors are used for increasing the disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAAA------AAAAA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1011 AAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841 ATTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGT----CCAACGTTTGAC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         723 AATACICCCICCGTITCAAAAIGITTGACACCGCIGATTITTTTTTTTTGTATGTTTGAT 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    898 CATTCGTCTTALTAAAAAAATTATGTATCTATTATTTATTTATTATGACTTGATTCGT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         783 CATTTGTCTTATTCAAAAAATTTAAGTAATTATTTATTATTTTTCGTATCATTTGACTCAT 842
Plant expression vector with pathogen-inducible regulatory element used for increasing disease resistance of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91.4; DB 18; Length 1591;
Pred. No. 5e-10;
0; Mismatches 71; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1591 BP; 464 A; 289 C; 373 G; 465 T; 0 other;
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ne : 777.159 secs
                                                                                                             Claim 1; Columns 11-14; 8pp; English.
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Matches 164; Conserv
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AQ051086 nbxb0005a
B1305800 NL_1_M15
BQ908458 T008E03 O
AU094078 AU094078
AU056564 AU056564
B1810180 J001B06 O
                                                                                              March 25, 2003, 19:50:00 ; Search time 2242.74 Seconds (without alignments) 15894.084 Million cell updates/sec
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                                                                                                                                                            US-09-702-134-7212_COPY_10200_12400
2201
1.ogtcgttcgttttgtgcatc......tagcttgtgcgttttgctgta 2201
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum DB seq length: 2000000000
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em_gss_fun:*
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2: em_esthum:*
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Perfect score:
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BM420118 R023H11 O BM420133 R024B0 O BQ908495 T008H05 O BE230875 99A8.79 R1 BM037750 S098C08 S BQ908635 T012B09 O BR911299 N00112 O BM038608 V006C02 O BM038608 V006C02 O BR906647 L010D02 O BR906647 L010D02 O BR911225 M001F09 O BR811225 W001F09 O BR812121 V009A06 O BM421616 V017011 O	BQ907480 P0070802 O C72803 C72803 Rice B1806502 S067001 S BE229715 985N0103 BQ280726 WHB3004_B BM038047 V003E10 O BM039048 V013F10 O BM42069 K023E08 O A4056563 BQ908614 T011G07 O BM19787 R018G06 O B1811322 N0016562	BM038823 V010C0C O BM038823 V010C0C O B18070C3 S082B0 S BC908540 T010B09 O B1810148 T005F07 O BF265938 HV_CEa001 BF265938 HV_CEa000 BF679710 949078B06 BF679710 949078B06 BF627121 HYSMED000 BF627121 HYSMED000 BF627121 HYSMED000 BF627121 HYSMED000 BF627121 HYSMED000	linear GSS 24-MAR-1999 yza sativa genomic clone 'Embryophyta; Tracheophyta; da; Poaceae;	ence the Rice Genome replaced gi:3325391.
	14 BQ9074 14 C72803 13 BE2297 14 BE2297 13 BM0390 13 BM0390 9 AU05650 14 BQ9086 14 BQ9086 14 BQ9086 13 BM4197		714 bp DNA CUGI Rice BAC Library Oryvons BAC Library Oryvons 1:4501804 ridiplantae; Streptophyta; Magnoliophyta; Magnoliophyta; Carvaea; Oryvae.	to Seguersion titute 634, US
443 20.1 522 19.6 534 9.4 19.5 534 9.6 19.0 6.8 18.9 623 44.4 18.1 539 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.4 17.7 576 9.5 17.7 576	7.6 17.2 16.4 17.2 16.4 16.4 17.2 16.4 16.4 16.4 16.4 16.4 16.4 16.4 16.4	23.000	AQ051086 nbxb0005acllr Cunbxb0005ezlr, DNAQ051086 AQ051086.2 GI:4 GSS. Oryza sativa. Oryza sativa. Bukaryota: Virid Spermatophyra: M	1 (bases 1 to 714) Wing, T.A. and Dean, R.A. Wing, T.A. and Dean, R.A. BAC End Sequencing Framework Unpublished (1998) On Mar 23, 1999 this sequence v Contact: Wing RA Clemson University Clemson University Clemson University Ou Jordan Hall, Clemson, SC 29 Tel: 864 656 4293 Fax: 864 656 4293
7 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		08040 - 0804040	RESULT 1 AQ051086 LOCUGS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE ATTHORS TITLE JOURNAL COMMENT

High quality sequence start: 31 High quality sequence stop: 250.

EST 20-JUL-2001

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta, Liliopsida; Poales; Poaceae, Ehrhartoideae, Oryzeae, Oryzea.
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                                                                                                                                                                                                                                                                                                                                              Oryza sativa cDNA clone NL 1 M15 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 633)
Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,
Ravindrababu,P. and Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
Stressed rice (Oryza sativa L.cv Nagina 22)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1413 ACGCCAGCATCGACCTCGCCTCCATCATCAAGAGGAAGCTCAGGAAGATCAAGGAGA 1472
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       599 AATIGGACCCTTAIGAAATACCTCTAGAATICAAATAAACTACAIGTCAICTCCAATIGCG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="NL_LM15"
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/dev_stage="35 day-old seedlings"
/note="Organ: Leaf; Vector: T773Pac; E9Ts from nor leaf conA library from drought stressed seedlings
159 c 187 g 162 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533 CATCGCTCGACGACGACGACGACGCCCAGGCCCAGCTCAAGGATCTGGAGGAGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.O. Central University, Hyderabad-500 046, A.P. India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Plant Sciences, School of Life Sciences University of Hyderabad
                                                                                                                                                                                                                                                                                                                         linear
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/organism="Oryza sativa"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="taxon:4530"
                                                                                                                                                            725 TATATT-AGTAGTAATTTGCTTCACTAGAATTCTATTTATAC 766
                                                                                                                                                                                        659 TATATICAGIGCGAAAICGCIGACTIAGACAICIATCIICIAC 701
                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arjulsleuchyd.ernet.in
Insert Length: 653 Std Error: 0.00
Plate: 1 row: M column: 15
Seq primer: GTARAACGACGGCCATTG.
Location/Qualifiers
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NL_1_M15 Drought stress (leaf)
MRNA sequence.
B1305800
                                                                                                                                                                                                                                                                                                                                                                                                               BI305800.1 GI:14981109
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Contact: Reddy AR
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Oryza sativa
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BI305800/c
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                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                      genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library onotains 36,864 clones with an average insert size of 128.5 KD providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                          /tissue_type="Leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBeloBAc11; Site_1: HindIII; Site_2:
/note="Vector: pBeloBAc11; Site_1: Airce is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics
                                                                                                                                                                                                                                                                                                                  and subtropics, rely on rice as their primary source of
earbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCAGCAATGGCCCTCGCCGCCTCCCTTCCCATCACCATCACCATGACCATGTCAAGC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GCGCCGTGTCCGTGCGGATGTCGTGGGACGGGCCCCTCTCCTCGGTCCGCCTCATTATG- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 CAGGGCCGCAACGTCCAAGGTTCTCCTCCTACTACCACTAGTTTGCTTCCCTGGAA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 ATGATAATATTCTAGATTCATTATCATATATATGATTATAGGTAATGCTAGAAAATCTTA 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GCAGAGCATTGTTCTTCTTCTAGCTATTAGTGGTGGGGAATAATGGCTCCCGGCCACCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GCGCCGTGTCCGTGCGGATGTCGTGGGACGGGCCCCTCTCCTCGGTCCGCCTCATTATGC 350
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                                                                                                                                                          /clone_lib="CUGI Rice BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 582.6; DB 17
Pred. No. 7.3e-109;
0; Mismatches 44;
                                              organism="Oryza sativa"
                                                                                             /cultivar="Nipponbare"
                                                                                                                /db_xref="taxon:4530"
/clone="nbxb0005E21r"
    Location/Qualifiers
                                                                      /strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.5%;
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Matches 654; Conservative
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474

/dev_stage="Mature stage" /note="Vector: pSport2" BASE COUNT 173 a 194 c 162 g 109 t ORIGIN Query Match 24.0%; Score 529; DB 14; Length 638; Best Local Similarity 89.0%; Pred. No. 6.7e-98; Matches 615; Conservative 0; Mismatches 0; Indels 76; Gaps 1;	QY 1365 CCAAGCGCCACGGCGTCATCCGCGCCGAGGACGCCGAGTCCACCTACGCCAGCATCG 1424 HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	1485 TCCGCCACCTCAAGGGACCAAGCCCCCGTCTCCGACTGGCCGCCATCATTGCTCGACA	Oy 1605 AccadeaccaderGeTCACCAGGTCTGCAGGTCTGATGCATGCATATAATCA 1664 Db 244 ACGAGGACAGGTGCTCACCA	QY 1785 TTCTACGCCTTCAGAGACGAGAAGACCGGGGAGATGAACGTCCTGTACAAGAGGAAGGA	QY 1905 AACTCTGACCACCCTCCCTTGCTGCTGCCTACACCTCCTGCATCACCTT 1964	OY 2025 TARICCAAGIGARGAGGCTTTGAIT 2055	TITION AU094078 Rice panicle at flowering stage Oryza sative cultivar-group) cDNA clone E2287, mRNA sequence. AU094078.1 GI:8856760 NN AU094078.1 GI:8856760 EST. AUSA sativa (japonica cultivar-group). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PoERCE I (bases 1 to 597) HORS Sasaki, T. and Yamamoto, K.
Db 473 TCGGCCGAGGACGAGGACACGGTGCTCACCA	1773 GIGGACCACAACTICTACGCCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1893 GAGACGARGGCACTTCGGTCCCCCAAGGGGGGCGTCTCCCCAAGGGGGGCGTCTCCCCAAGGGGGGGCTCTCCTCCCTGCCTG	2013 ACTAGTATTA -129 ACTAGTATTA -129 ACTAGTATTA 2073 ATGGATGGAC 69 ATGGATGGAC 2133 TGATTTTC	9 TGATTTTC 1 3 8 BQ908458 ION T008803 GTYZ ON BQ908458	VERSION BQ908458.1 GI:22307236 KEYWORDS BST. SOURCE Oryza sativa. ORGANISM Oryza sativa. ORGANISM Oryza sativa. SUBARCE Oryza sativa. Spermatophyta; Maynoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Maynoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. REFERENCE 1 (Dases 1 to 638)	ω H	Tel: 0086-571-86892051 Fax: 0086-571-86961525 Email: htdong@zjuen.zju.edu.cn Seq primer: M3 forward primer. Location/Qualifiers 1. 638 /organism="Oryza sativa" /clone="10048xon:4530" /clone="10048xon:4530" /clone="10048xon:4530" /clone="100-"Oryza sativa mature leaf library induced by M.grisea" /tissue_type="leaf"

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Query Match
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SOURCE
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Matches
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/dev_stage="flowering stage"
/note="organ: paniele; Rice cDNA from paniele at flowering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Taxiii Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
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/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Rice cDNA from panicle at flowering stage (2000) Unpublished (2000)
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                                                                       Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsesaki@abr.affrc.go.jp,
PROJECT = FRGP',
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Location/Qualifiers
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87.7%;
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AU056564 Oryza sativa mature leaf Nipponbare Oryza sativa (japonica au056564 Oryza sativa sequence.
AU056564 Grand Sequence.
BST. 01.4715447
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 570)

Yamamoto, K. and Sasaki, T.

Rice cDNA from mature leaf

Unpublished (1999)
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llarity 98.7%; Pred. No. 1.6e-81;
Conservative 0; Mismatches 6; Indels
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2,
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
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RESULT 6

RESULT 5

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BM420118 1002 activa mature leaf library induced by M.grisea Oryza sativa clone R023H11, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 52)
Dong, H.T., Li,D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
| Ough_xref="taxon:4530" |
| Allone="R034Hl" |
| Clone=lib="Oryza sativa mature leaf library induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2037 TGAGAGGECTTTGATTTTGTCTCCGTGTACATCGATCGACTCTTGACTACTCTG 2096
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Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Fax: 0086-571-8699051
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11 Similarity 100.0%; Pred. No. 2.6e-80;
443; Conservative ' 0; Mismatches 0;
                                                                                            2097 ITTAACCAACTGTTTTCGATATATTTATATTAT 2132
                                                                                                                TITAACCCACTGITITICGAIAAAAAAAAAAAAAAAA 574
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/note="Vector: pSport2"
136 c 122 g 126
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Seq primer: M13 forward primer.
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/tissue_type="leaf"
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BM420118.1 GI:18386920
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                  EST 02-0CT-2001
                BI810180 575 bp mRNA linear EST 02-OCT-2001 5001B06 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone J001B06, mRNA sequence.
                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryzaeae; Oryzaeae; Oryzaeae; Dong, H.T., Lil,D.B., Zhuang, X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Goo,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
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/organism="oryza sativa"
/db_xref="txon:4530"
/clone="001806"
/clone_lib="oryza sativa mature leaf library induced by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TC-GTGGAGGAGTCGATGGAGCACGCTAGTGAATGTGGACCACAACTTCTAGGCTTCAG
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                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Context: Dong HT
Context: Dong HT
Context: Dong HT
Context: Dong Institute of Lhejiang University
Kaixuan Road Z68#, Hangzhou, Zhejiang, P.R.China
Fax: 0086-571-869961525
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers
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                                                                             BI810180
BI810180.1 GI:15857368
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                                                                                                                                Oryza sativa.
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90908495 525 bp mRNA linear EST 19-AUG-2002 1008H05 Oryza sativa mature leaf library induced by M.grisea Oryza
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1 (bases 1 to 525)
Dong-H.T., Lil-D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
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                                                               2002 CTCTAAATATTAC-TAGTATTAATTAATCCAAGTGATGAGAGAGGGCTTTGATTTGTCT 2060
                                                                                                                                            2061 CCGIGTACATCGATCGACTCTTGACTACTCTGTTTAACCAACTGTTTTCGATATAT 2120
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                                                                                                    378 CICIAAATAITACGIAGIATAATIAATICCAAGIGAIGAGAGAGAGGICITIGAITTIGICI 437
                                                                                                                                                                 Query Match 19.5%; Score 429.4; DB 14; Length 525; Best Local Similarity 99.3%; Pred. No. 1.6e-77; Matches 441; Conservative 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Raixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86981251
Fax: 0086-571-86961525
Bmail: htdong@zjuem.zju.edu.cn
Seq primer: MJ3 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                         sativa cDNA clone T008H05, mRNA sequence
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/dev_stage="Mature stage"
/note="Vector: pSport2"
134 c 120 g 128
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/db_xref="taxon:4530"
/clone="T008H05"
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Organ sativa.

Organ sativa

Organ sativa

Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.

1 (Dasses 1 to 534)

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, O.K. and Lou, Y.C.
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/clone="R024506"
/clone_lib="Oryza sativa mature leaf library induced by
                                                                               2062 CGTGTACATCGATCGACTCTTGACTACTCTGTTTAACCAACTGTTTTCGATATATT 2121
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                       78 AGGIGGIGCIGCACCAAGGIGITCGAGAIGCCGCCGCTGTCGGIGGAGGCGAIGGAGC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
CTCTAAATATTACTAGTATTAATTCCAAGTGATGAGAGAGGTCTTTGATTTTGTCTC
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Bio-technology Institute of Zhejiang University
Kaixuan Road Z68#, Hangzhou, Zhejiang, P.R.China
11. 0086-571-86991535
Fax: 0086-571-86961525
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0; Mismatches
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/dev_stage="Mature stage"
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139 c 127 g 1
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Seg primer: M13 forward primer.
Location/Qualifiers
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BM420133.1 GI:18386935
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Best Local Similarity 99.8%;
Matches 443; Conservative
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JOURNAL
COMMENT
  2002
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AUTHORS
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                                                                                                                                                                                                                                                            RESULT 8
BM420133
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KEYWORDS
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/clone_lib="Stem library from Oryza sativa (3-5 leaf stage
                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryzea.

1 (Dases 1 to 62?)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Janag, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
Jene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1762 AGCTAGTGAATGTGGACCACACATTCTACGCCTTCAGAGACGAGAAGACCGGGGGAGATGA 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1702 AGGIGGIGCGCACCAAGGIGITCGAGAIGCCGCCGCTGTCGGIGGAGGAGGCGAIGGAGC 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AGCTAGTGAATGTGGACCACAACTTCTACGCCTTCAGAGACGAGAAGAACGGGGGAGATGA 294
                                                                                                                        CCACCACCACCAGCAATGGCCCTCGCGCCTCCTTCCCATCACCATCACCATCACCATG 240
                                                                    191 CCACCACCGCAGCAATGGCCCTCGCGCCGCCTTCCCATCACCATCACCATG 250
                                                                                                       TCAAGCAGCTGCAGCTCCCTCCGTCTGTCTTCCGTCTCCGTGCCCCTCCGGTTCCGGTTTCC 300
                                                                                                                                                                          ITGGCCGCGCACTGCTGCTGCTGCCACCCACACCGCTGCTCGCCGCCGAGAGCCGCC 360
                                                                                                                                                                                                                                              GCAGCAGCGCCGTGTCCGTGCGGATGTCGTGGGACGGGCCCCTCTCCTCGGTCCGCCTCA 420
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GCGAGAGCAGAGCATTGTTCTTCTTCTAGCTATTAGTGGGGGAATAATGGCTCCCG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sativa (3-5 leaf stage) Oryza sequence.
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Pred. No. 6e-75;
0; Mismatches 2; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Confect: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Bio-technology Institute of Zhejiang University
Tel: 0086-571-86892051
Fax: 0086-571-8699125
Fax: 0086-571-86961525
Fax: 0086-571-86961525
Seq primer: M13 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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/dev_stage="3-5 leaf stage"
/note="Vector: pSport2"
171 c 145 g 150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="S098C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           S098C08 Stem library from Oryza sativa cDNA clone S098C08, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           627 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         TTATGCAGGGCGGAACGTCAAGCT 454
                                                                                                                                                                                                                                                                                                                    421 TTATGCAGGCCGCAACGTCAAGGT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM037750.1 GI:16753371
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa.
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Best Local (
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JOURNAL
COMMENT
131
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BM037750
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/clone=11b="Rice Seedling Lambda ZAPII CDNA Library"
/dev_stage="5 day Safter Pollination"
/lab_nost="e. col; SOLR"
/lab_nost="col; SOLR"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Vector at S'end with EcoRI and 3' end with Xho I site"

161 c 111 g 107 t
                                                                                                                                                                                                                                                                                                                                                                        EST 07-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Engrayota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                    BE230575 460 bp mRNA linear EST 07-JUL-20 99AS79 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa cDNA clone 99AS79, mRNA sequence.
                                   CCICTACACCICCIGCAICACCAICCICAITIGCIAATTAITICIAIGCIIGCCAAGAG 2000
                                                                                                     2001 TCTCTAAATATTACTAGTATTAATTAATCCAAGTGATGAGAGAGGGTCTTTGATTTTGTCT 2060
                                                                                                                                                                          2061 CCGTGTACATCGATCGACTCTTGACTACTCTTTAACCAACTGTTTTCGATATAT 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 CCGIGTACATCGATCGATCGATCTCTTGACTTATAACCAACTGTTTTCGATATAT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAGCTTCTCTCTCTTCTTTAAGAGCAAGCAAACAGTAGTCTAGCGAAAGCGAGACT 120
1 (bases 1 to 460)
Lee, M.C., Shin, Y.C., Lee, T.H., Jeong, S.H., Kim, J.K., Bun, M.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Cytogenetics
Mational Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 418.6; DB 1
Pred. No. 2.6e-75;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .460
/organism="Oryza sativa"
/cultivar="Milyang23"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                              TTATATTATTATGATTTTTCCAA 2144
                                                                                                                                                                                                                                                                 TTATATTATTAATGATTTTTCCCA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                             BE230575.1 GI:8956772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Eun M.Y.
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Best Local
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AUTHORS
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BE230575
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JOURNAL
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BI811299 516 bp mRNA linear EST 02-0CT-2001 N001C12 Oryza sativa mature leaf library induced by M.grisea Oryza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Oryza sativa mature leaf library induced by M.grisea"
1771 ATGIGGACCACAACTICTACGCCTICAGAGACGAGAAGACCGGGGGAGAIGAACGICCIGI 1830
                                                                        1831 ACA-AGAGGAAGGAAGGCTTCGGTCTCATCGTCCCAAGGGAGACGGTCATCTCCCAC 1889
                                                                                                                                              CTCCTGCATCACCATCCTCATTTGCTAATTATTTCTATGCTTGCCCAAGAGTCTCTAAAT 2009
                                                                                                                                                                                                                                                                                                2010 ATTACTAGTATTAATTAATCCAAGTGATGAGAGGGGTCTTTGATTTTGTCTCCGTGTACA 2069
                                                                                                                                                                                                                                                                                                                                                                      1701 CAGGTGGTGCGCACCAAGGTGTTCGAGATGCCGCCGCTGTCGGTGGAGGAGGCGATGGAG 1760
                                                                                                                                                                   241 CTCCTGCATCACCATCCTCATTTGCTAATTATTTCTATGCTTGCCCCAAGAGTCTCTGAAAT 300
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Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Fax: 0086-571-869961525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 410; DB 13;
Pred. No. 1.5e-73;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sativa cDNA clone N001C12, mRNA sequence.
BI811299 GI:15858487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="leaf"
/dev_stage="Mature stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /orqanism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pSport2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers
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/clone="N001C12"
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98.2%;
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Best Local Similarity 98.2
Matches 436; Conservative
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ORIGIN
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BI811299
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KEYWORDS
SOURCE
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District Straight Streptophyta; Embryophyta; Tracheophyta; Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperardophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enhartoideae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.T., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.

A Gene Expression Screen in Oryza sativa
Unpublished (2001)
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               1822 ACGICCIGIACAAGAGGAAGGAAGGCTICGGTCICAICGICCCCAAGGGAGACGGIC 1881
                                                                                       1941 CCTCTACACCTCCTGCATCACCATCTTGCTAATTATTTCTATGCTTGCCCAAGAG 2000
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                                      295 ACCTCTGTACAAGAGGAAGGAAGGCTTCGGTCTCATCGTCCCCAAGGGAGACGGTC 354
                                                                                                             355 AICTCCACCAAGGAGACCAICCCCAACTCTGACCACCACCACCCTTGCTTGCTGCTAG 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Fax: 0086-571-8699051
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/note="Vector: pSport2"
113 c 93 g 115
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Seg primer: M13 forward primer.
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L010D02 Oryza sativa mature leaf library induced by M.grisea Oryza sativa clone L010D02, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 531)
Dong, H.T., Li,D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.T., Jiang, Y.X., Yu, F.C., Gao, O.K. and Lou, Y.C.
Unpublished (2001)
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/db_xref="taxon:4530"
/clone="r.010002"
/clone_lib="Oryza sativa mature leaf library induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2012 TACTAGTATTAATTAATCCAAGTGATGAGAGGGTCTTTGATTTTGTCTCCGTGTACATC 2071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1952 CCTGCATCACCATCCTCATTTGCTAATTATTTCTATGCTTGCCCAAGAGTCTCTAAATAT 2011
                                                               1712 CACCAAGGIGTTCGAGATGCCGCCGCTGTCGGTGGAGGAGGCGATGGAGCAGCTAGTGAA 1771
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                                                                                                                                                                                                                                                                                                                  1832 CAAGAGGAAGGAAGGAGGTTCGGTCTCATCGTCCCCAAGGGAGACGGTCATCTCCACAA 1891
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                                                                                                   118 TGTGGACCACAACTTCTACGCCTTCAGAGACGAGAAGACCGGGGAGATGAACGTCCTGTA, 207
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Laboratory of Functional Genetics
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Tel: 0086-571-8682051
Fax: 0086-571-86961525
Fax: 0086-571-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 t
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/dev_stage="Mature stage"
/note="Vector: pSport2"
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1 (Dases 1 to 539)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, A.R., Zhang, Y.X., Yu, F.C., Gao, Q.X. and Lou, Y.C.

A Gene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM038608 100-NOV-2003 539 bp mRNA linear EST 06-NOV-2003 V006C02 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone V006C02, mRNA sequence.
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                                                                                                1761 CAGCTAGTGAATGTGGGACCACAACTTCTACGCCTTCAGAGACGAGAAGACCGGGGAGATG 1820
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   1821 AACGTCCTGTACAAGAAGGAAGGAGGCTTCGGTCTCATCGTCCCCAAGGGAGACGGT
                                                                                                                                                                                                                                                                                       174 AACGICCIGTACAAGAGGAAGGAAGGAGGCITCGGICTCAICGICCCCAAGGGAGACGGI
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Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Pax: 0086-571-86961525
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/dev_stage="Mature stage
/note="Vector: pSport2"
a 144 c 117 g 13
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Seq primer: M13 forward primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 TTATATTATTAATGATTTTTCCCA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM038608.1 GI:16754229
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97.5%;
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Best Local Similarity
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE COMMENT

DEFINITION

LOCUS

ACCESSION

RESULT 14 BM038608

2121

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2061

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FEATURES

BASE COUNT ORIGIN

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1;
                                                           1702 AGGTGGTGCGCACCAAGGTGTTCGAGATGCCGCTGTCGGTGGAGGAGGCGATGGAGC 1761
                                                                                                                 ACGTCCTGTACAAGAGGAAGGAAGGAGGCTTCGGTCTCATCGTCCCAAGGGAGGACGGTC 1881
                                                                                                                                                                                                                                      1942 CTCTACACCTCCTGCATCACCATCCTCATTTGCTAATTATTTCTATGCTTGCCCAAGAGT 2001
                                                                                                                                                                                                                                                                                                                                                       2002 CTCTAAATAITACTAGTATTAATTAATCCAAGTGATGAGAGGAGGTCTTTGATTTTGTCTC 2061
                                                                                                                                                                                                                                                     219 ATCICCACAAGAGAGACCATCCCCAACTCIGACACCACCACCCCTCCCTTGCTGCTGCCTAGC 278
                                                                                                                                                                                           279 CICTACACCTCCTGCATCACCATCCTCATTACTTATTTCTATGCTTGCCCAAGAGT 338
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                            40 AGGTGCTGCGCACCAAGGTGTTCGAGATGCCGCC-CTGTCGGTGCAGGAGGCGATGCAGC 98
                                ij
Score 397.4; DB 14; Length 531;
Pred. No. 5.6e-71;
0; Mismatches 1; Indels 1;
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99.5%;
               Best Local Similarity 99.59
Matches 409; Conservative
 Query Match
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Search completed: March 26, 2003, 07:52:29 Job time: 2267.4 secs

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March 26, 2003, 04:38:30; Search time 54.4409 Seconds (without alignments) 12398.686 Million cell updates/sec
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2201
1 cgtcgttcgttttgtgcatc......tagcttgtgcgttttgctgta 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 3, Appli	,	14	Sequence 14, Appl	Sequence 1137, Ap	m	'n	Sequence 3, Appli	186	-		Sequence 209, App		4	13	36,	288,	19,	Sequence 4, Appli	Sequence 2, Appli	13	Sequence 1, Appli	Sequence 786, App	m	Sequence 13, Appl	Sequence 2, Appli	Sequence 40, Appl
	ΠD	US-08-728-956-3	US-09-105-390-3	US-08-232-463-14	US-08-232-463-14	US-08-998-416-1137	US-08-728-956-3	US-08-581-148C-3	US-09-105-390-3	US-08-998-416-186	US-09-197-649-7	US-08-998-416-288	US-08-781-891-209	US-08-213-419B-3	US-09-023-173-4	US-08-487-826B-13	US-08-883-795A-36	US-08-998-416-288	US-09-385-028-19	US-09-249-585A-4	US-09-130-114-2	US-09-385-028-13	US-09-385-028-1	US-08-998-416-786	US-09-144-085-3	US-08-487-826B-13	US-09-124-541-2	US-09-105-537-40
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	Query Match Length DB	1591	2317	7218	7218	636	1591	1138	2317	615	390	837	51259	6124	1140	19124	999	837	1182	1926	1931	11604	15079	711	33529	19124	6733	2787
οψ	Query	4.2	3.7	3.5	3.4	2.8	2.8	2.7	2.7	2.7	5.6	2.5	2.4	2.3	2.3	2.3	2.3	2.2	2.5	2.2	2.2	2.3	2.5	2.3	2.5	2.5	2.5	2.5
	Score	91.4	80.8	77	74.2	62.2	61.8	59.6	58.8	58.4	56.6	56	52.8	51.2	50.8	50.6	20	49.2	49.2	49.2	49.2	49.2	49.2	49	49	48.4	48.2	48
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Gaps

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841 ATTACTACCTCCATATTTAATGTATGACGCCGTTCACTTTTTGT---CCAACGTTTGAC 897

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Query Match
Best Local Similarity 66.9%; Pred. No. 8.4e-12;
Matches 164; Conservative 0; Mismatches 71; Indels 10

Sequence 21, Appl sequence 518, Appl sequence 538, Appl Sequence 1, Appl sequence 1, Appl sequence 1, Appl sequence 14, Appl Sequence 2, Appl Sequence 4, Appl Sequence 2, Appl Sequence 2, Appl Sequence 4, Appl Sequence 4, Appl Sequence 2,	,	
28 48 2.2 5970 3 0S-09-320-878-21 c 29 47.8 2.2 12730 4 0S-09-004-838-91 c 31 47.8 2.2 4403768 4 0S-09-004-838-91 32 47.6 2.2 1072 1 0S-07-971-096-1 34 47.6 2.2 1072 1 0S-07-971-096-1 34 47.4 2.2 168575 4 0S-08-426-290-1 35 47.4 2.2 168575 4 0S-07-951-715A-14 37 47.4 2.2 3546 1 0S-07-951-715A-14 38 47.4 2.2 3546 3 0S-08-459-448A-14 41 47 2.1 3468 1 0S-07-951-715A-2 42 47 2.1 3468 1 0S-07-951-715A-4 43 47 2.1 3468 2 0S-08-459-448A-4 44 47 2.1 3468 2 0S-08-459-448A-4 45 47 2.1 3468 2 0S-08-459-448A-4 46 47 2.1 3468 2 0S-08-459-448A-4 47 2.1 3468 2 0S-08-459-448A-4 48 47 2.1 3468 2 0S-08-459-448A-4	ALIGNMENTS	RESULT 1 US-08-728-956-3 Sequence 3, Application US/08728956 Fatter No. 5677175 GENERAL INFORMATION: APPLICANT: Hodges, Thomas K. APPLICANT: McGes, Thomas K. APPLICANT: McGes, Thomas K. APPLICANT: McGes, Thomas K. APPLICANT: McGes, Thomburg STREET: 11 S McFidian CITY: Indianapolis STREET: 11 S McFidian CITY: Indianapolis STREET: UGA ZIP: Hodges FORM: MEDIUM TYPE: Floppy disk COMPTER: UGA ZIP: PatentIn Release #1.0, Version #1.30 OPERATING SYSTEM: PC-005/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DAR: APPLICATION NUMBER: US/08/728,956 FILLING DATE: PATORNEY APPLICATION NUMBER: 3220-26119 TELEPHONE: John P. REGISTRATION INFORMATION: NAME: Breat, John P. REGISTRATION INFORMATION: TELEPHONE: (317)231-7745

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1009 AAAAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAG 1068
                                                                                                                                    1069 GGATTATATGGGATAGCTACAGTAGCAGAGTCATGATAAAGTAGTAATGTGTTGGGAGGA 1128
   799 TAAGACAAACGGTCAAACATGTTCTAAAAGTCAAGGGTGTCAAACATTTTGAAACGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Foley & Lardner: 1800 Diagonal Road, Suite 500 Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; CLONE: pTZgpt-Fls
US-08-232-463-14
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                          Patent No. 5670367 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                    US-08-232-463-14/C
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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COUNTRY:
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                                                                                                                                                                                                             1011 AAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTGATACATTAAAATACGGAGGG 1070
                                                                                                                                    CATCAAATATTTTTTAAGCATGACATAAACATTTTCATATTTGCAAAA-----AAAAA 1010
                                                                                                                                                                                                                                   896 ACCATTCGTCTTATAAAAAAATTATGTATCTATTATTATTATTATTATGACTTGATTC 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          919 ACCATITGECITATECAAAAATTAAGTAATTATTATTATTATETTETTEATGATEC 860
                                                                                                                                                                       843 IGTTAAATATACTTTCAIGTGCACATATAGTTTTACATATTTCACAAATTTTTGAATA 902
783 CATTTGTCTTATTCAAAAAATTTAAGTAATTATTATTATTATTTTCGTATCGTTTGACTCAT 842
                                                           8
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Pred. No. 2.8e-09;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Rice Beta-Glucanase Enzymes TITLE OF INVENTION: and Genes OF INVENTION: and Genes CORRESPONDENCE: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/105,390 FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60/050,675
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09105390 Patent No. 6288303
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.7%;
nilarity 64.6%;
Conservative 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 500 CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                      1071 ATTAT 1075
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US-09-105-390-3/c
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US-09-105-390-3
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Matches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1016 AATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTAT 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 3.5%; Score 77; DB 1; Length 7218; 1 Similarity 6.9%; Pred. No. 3.7e-08; 23; Conservative 201; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.25
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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309
                   190 CAGCAATGGCCCTCGCCCCCTCCTTCCCCATCACCATCACCATCACCATGTCAAGCAGC 249
                                                                                                                                                                  310 CACTGCCTGCTGCTGCCCACCCACGCTGCTCGCCGCCGAGAGCCGCCGCAGCAGCAGC 369
                                                                                                                                                                                                                                         370 CCGTGTCCGTGCGGATGTCGTGGGACGGGCCCCTCTCCGGTCCGCCCTCATTATGCAGG 429
                                                                                                                                                                                                                                                                                                                  430 GCCGCAACGTCAAGGTTCTCCTCTTACTGCTACCACTAGTTTGCTTCCCTGGAATTTC 489
                                                                                            250 TGCAGCTCCCTCCGTCTGTCTCCGTCTCCGTGCCCTCCGCTCCGGTTTCCTTGGCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                  1424 YYYYYYYYYYYYGDACCAAATTCTTCTATCTTTAACTACTTGCATAGATAGGTA 1478
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rebischung, Corine
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSIPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1137, Application US/08998416
Patent No. 6239264
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
RILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPERENCE/POCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPROX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSE: NO. 62392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-998-416-1137
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APPLICANT:
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                       1196 GIGGCGGIGCAGCIGAATGAGAAGGIGAAGGAGCACAICGAGGAGAAGGCGGGGAGAGCA 1255
                                                                                                                                                                        130 GAGCATTGTTCTTCTTCTTCTAGCTATAGTGGTGGGGGAATAATGGCTCCCGCCACCACCACCG 189
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1 Similarity 6.0%; Pred. No. 1.6e-07;
25; Conservative 236; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFWMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: TAKENER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                       1256 GIGGCGAAGCACAGCCAGCTIGIGAAGGAGGIGGA 1290
                                                                                                                                                                                                                                                     30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERBNCE/DOCKET NUMBER: 3047;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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STATE: VE
COUNTRY: USA
--. 22313-0299
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US-08-232-463-14
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REGISTRATION NUMBER:
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TOPOLOGY: lir
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ANTI-SENSE: N
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                                                                                                                                                                                                                                                 560 GATTCATTATCATATATATGATTATAGGTAATGCTAGAAAATCTTATAACCTGAAACAGA 619
                                                                                                                                                                                                                                                                                       198 --TTAATATGAATACTATTTAGTCTATGTTCAAATTTTAAATTTAGTTATTAAAATATTAT 255
                                                                                                                                                                                                                                                                                                                            620 GGGAGTATATATAATTCGGTAATGGAACTAGAGTATTTGTTTTATTAATTGGACCTTTAT 679
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                                                                                                                                     3;
                                                                                                  Length 636;
                                                                                              Score 62.2; DB 4; Length 63
Pred. No. 3.1e-05;
0; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08728956
Patent No. 5677175
GENERAL INFORMATION:
APPLICANT: McGee, J. D.
TITLE OF INVENTION: Plant Pathogen Induced Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/728,956
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STREET: 11 S Meridian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
     DNA (genomic)
                                                                                                2.8%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
                                                                                              Query Match 2.8'
Best Local Similarity 46.8'
Matches 230; Conservative
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                                       PAG1692RP
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MOLECULE TYPE: DI
ORIGINAL SOURCE:
ORGANISM: PAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 46204
                                                          US-08-998-416-1137
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996 AITIGCAAAAAAAAAAACGAAIGGICAAAIGITAGICGAAAAGICAAIGGIGICAIACA 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     946 GACTTGATTCGTCATCAAATATTTTTAAGC------ATGACATAAACATTTTCAT 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.8; DB 1; Length 1591;
Pred. No. 5.9e-05;
0; Mismatches 107; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nikolau, Basil J.
APPLICANT: Xu, Xiaojie
APPLICANT: Xu, Xiaojie
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
                      3220-26119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/581,148C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Schnable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  743 TTTTGAAACGGAGGGAGTATTTG 721
38,833
                   REFERENCE/DOCKET NUMBER: 32.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)231-7745
TELEFAX: (317)231-7433
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.8%;
Best Local Similarity 55.5%;
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
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                                                                                                                                                                               LENGTH: 1591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Oryza sativa
US-08-728-956-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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945 TGACTTGATTCGTCATCAAATATTTTTTAAGCATGACATAAACATTTTCATATTTGCAAA 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      825 TAIGGACCTAITACITAITACTACTCCCATATITIAAIGIAIGACGCCGITCACTITITG 884
                                                                                                                                                                                                                                                           Length 2317;
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                                                                                                                                                                                                                                                                                                           Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                             Score 58.8; DB 4;
Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSEE: No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
TITLE OF INVENTION: GENOMIC DNA
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U5/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 43:5
PRIOR APPLICATION DATA:
FILING DATE: 31-DEC-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 186, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3054 Convallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
  FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                               2.78;
                                                                                  INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1152
                                                                                                                                                                                                                                                             Query Match 2.7
Best Local Similarity 57.7
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                           TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                        ; TOPOLOGY: linear
US-09-105-390-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-998-416-186
                         TELEPHONE:
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896 AA 897
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APPLICANT:
                                                                     TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1495 CAAGGGGACCAAGCCCCCCGTCTCCGACTGGCCGCCATCATTGCTCGACAACAACGACGA 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1555 GGAGGCCCAGGCTCAAGGATCTGGAGGAGCCGTCGGCGCCGAGGACGAGGACAC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 GATCAGGGCCAAGTACCCAAGACCGAGGTCCGCCTCGTGCTCGACTTCGCCTCCGA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 GGGCTCGCCCCGGGGTGGAGGCGCTCAAGGACTCCATCCGGGGCCTCGACGCGT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 CGTCGTCACCGGCCCACCGACGGCATCGGCCGCCATCGCCTTCCGCCTCGCCGTC 294
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                                                                                                                                                                                                                                                                                                                                                2.7%; Score 59.6; DB 3; Length 1138; 51.9%; Pred. No. 0.00016; tive 0; Mismatches 124; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
APPLICANT: ROCATIONEZ, RAYMONG
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
TITLE OF SEQUENCES: 66
CORRESSED Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION NUMBER: US/09/105,390 FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Petithory, Joanne R. REGISTRATION NUMBER: P42,995 REFERENCE/DOCKET NUMBER: 2000-0455.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NOBABR: 60/050,675
FILING DATE: 25-UDN-97
ATTORNEY/AGENT INFORMATION:
      RAGISTRATION NUMBER: 35243
REGISTRATION NUMBER: 35243
REPERRINGE/DOCKET NUMBER: 7138(
TELEPHONE: (312) 616-5600
INFORMATION FOR EQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1138 base pairs
                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1615 GGTGCTCACCAAGGTCTG 1632
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 51.9
Matches 134; Conservative
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                                                                                                                                                                                      LENGTH: 1138 base pai
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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US-09-105-390-3
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Philippsen, Peter
Pohlmann, Rainer
ORGANISM: Artificial Sequence
                                                                                                                                 Query Match
Best Local Similarity
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                                 OTHER INFORMATION:
OTHER INFORMATION:
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US-08-998-416-288
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APPLICANT:
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                                                                             ; OTHER INFOR
US-09-197-649-7
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APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXO2/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CORRENT FILING DATE: 1998-11-23
EARLIER RILING DATE: 1998-11-3
EARLIER RILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER APPLICATION NUMBER: 07/739,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                680 GAAAIACTAGIAGAATICAACGAAACTACATTCTICTTTATIGGTTATTAGIAGIAAT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 ТТАПТААТПСТТТАТТАААТААТАТАТТТТТТАТТАТТАТААСАТТТАДТТТАТТАТАТТ 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           920 TATGTATCTATTATTATTTATGACTTGATTCGTCATCAAATATTTTTAAGCATG 979
                                                                                                                                                                                                                                                                                                    560 GATICATIAICATATATATATATATAGGTAAIGCIAGAAAAICTTATAACCIGAAACAGA 619
                                                                                                                                                                                                                                                                                                                                                                                                                  198 --TTAATATGAATACTATTTAGTCTATGTTCAAATTTTAAATTAGTTATTAAATATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 TIATTTAACTTTTAAGAATTATTAAAAATTAATTTTAACTTTAATTTCTTAITAT 494
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                                                                                                                                                                                                                               Length 615;
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                                                                                                                                                                                                                             Score 58.4; DB 4; I
Pred. No. 0.00023;
0; Mismatches 246;
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EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09197649
Patent No. 6194550
BERERAL INFORMATION:
APPLICANN: Gold, Larry
APPLICANT: Tuerk, Craig
                 186:
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                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                             Query Match 2.7%;
Best Local Similarity 47.9%;
Matches 230; Conservative
             INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHRRACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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919-541-8689
                                                                                                                                                                   ; ORGANISM: PAG1074RP
US-08-998-416-186
TELEFAX:
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1552 CGACGACGCCCAGGCCCAGCTCAAGGATCTGGAGGAGGGCCGTCGGCGCCGAGGACGAGGA 1611
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                                                                                                                                                                                                                                                                                                                                                                                                             CTCCTCCATCATCAAGAGGAAGCTCAGGAAGATCAAGGAGAAGGAGACCGACGTCCGCCA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCAAGGGGACCAAGCCCCCGTCTCCGACTGGCCGCCATCATTGCTCGACAACAACGA 1551
                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Wohr, Christine
APPLICANT: Wondland, Jurgen
APPLICANT: Renchle, Philipp
APPLICANT: Rechischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSED: No. 6239264artis Corporation
STREET: 3054 Cornwalls Road
CITT: Research Triangle Park
Description of Artificial Sequence: Sequence having a 120 repeat of ACG flanked by fixed fragments having Ncol restriction sites.
                                                                                                                                                         Query Match 2.6%; Scoré 56.6; DB 4; Length 390; Best Local Similarity 51.0%; Pred. No. 0.00048; Matches 134; Conservative 0; Mismatches 129; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPOTER: IBM PC COMPATIBLE
OPERATUR SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGBNT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 288, Application US/08998416 Patent No. 6239264
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFRATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/781,891
FLING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPRONE: (206) 622-4900
TELEPRA: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                        ATTORNET AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08213419B Patent No. 6333406
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ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.4%;
Best Local Similarity 47.1%;
Matches 162; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Ver. 2.0
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US-08-781-891-209
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LENGIH: 6124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 --TTAATATGAATACTATTTAGTCTATGTTCAAATTTTAAATTAGTTATAAATTATTAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 GGGAGTATATATAATTCGGTAATGGAACTAGAGTATTTGTTTTATTAATTGGACCTTTAT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 GAAATACTAGTAGAATTCAACGAAACTACATTCTTCTTTATTGGTTATTAGTAGTAAT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 TIATTAATTGTTTAATAAATAATATTTTTTTATAAAAGATTTAATTAATTAAAT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATACCCGTTGCAACGGAATAGTAATATGGACCTATTACTTATTACTACCTCCATATT-T 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 TAPTITAATCTITITATAAGAATTATTAATAAATTAATTITAACTITAATTTCTTATTAT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         919 ITAIGIAICIATITATITATITATARACTIGATICGICAICAAATATITITAAGCAI 978
                                                                                                                                                                                                                                                                                                                          740 TIGCTICACTAGAATICTATITIATACTAGAGATTAAAAATTATTACAAAACTAACIG 799
                                                                                                                                                                                                                                       2.5%; Score 56; DB 4; Length 837; ilarity 47.4%; Pred. No. 0.00095; Conservative 0; Mismatches 255; Indels
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Patent No. 6090620

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Fu, Chang-En

APPLICANT: Wi, Chang-En

APPLICANT: Willigan, John T.

APPLICANT: Schellenberg, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO

TITLE OF INVENTION: WERNER'S SYNDROME

NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
    288:
                                                                                                                                    DNA (genomic)
                                        LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
    INFORMATION FOR SEQ ID NO:
                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
                                                                                                                                                                          ; ORGANISM: PAG1241RP
US-08-998-416-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               979 GACATAAACATT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616 GTAGTTAAAAT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 233; Conserva
                                                                                                             linear
                                                                                                       TOPOLOGY: linea
MOLECULE TYPE: DN
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-781-891-209/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Inselburg, J. et al.
TITLE OF INVENTION: GENE ENCODING PROPEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
TITLE OF INVENTION: AND USES THEREFOR
CURRENT APPLICATION WUMBER: US/08/213,419B
PRIOR PLING DATE: 1994-03-14
PRIOR FILING DATE: 1992-04-17
NUMBER OF SEQ ID NOS: 20
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                                                                                                                                947 ACTTGATTCGTCATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAAAA 1006
                                                                                                                                                                                                                                                                                                                                                                                           1067 AGGGATTATATGGGATAGCTACAGTAGCAGAGTCATGATAAAGTAGTAATGTGTTGGGAG 1126
                                                                                                                                                                                                                                                             1007 AAAAAAACGAAIGGICAAAIGIITAGICGAAAAGICAAIGGIGICAIACAIIAAAAIACGG 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1127 GAGCGGTAGAGCGTTGTGTGGAAAAAAAAGATGGGAATGGAATGAAAGCGTAC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1187 GTGCGTGGCGTGGCGGTGCAGCTGAATGAGAAGGTGAAGGAGCACATCGAGGAGAAGGCG 1246
                                                                                                                                                                         286 CTARARCACARCARTRCATGRAGARGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 AAACACACAATAAGAAATCCAGACCCTGTAAATGATTGAATGAGTAAAACACAGAATGT
Score 52.8; DB 3; Length 51259;
Pred. No. 0.037;
0; Mismatches 182; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1247 GGGAGAGCAGTGGCGAAGCACAGCCTTGTGAAGGAGGTGGA 1290
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NAME/KEY: CDS
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GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Willems, Thomas E.
TILLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1353 TCACTCTCTCACCAAGCGCCACGGCGTCATCCGCGCGAGGAGGACGCCGAGTCCACCT 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1533 CATTGCTCGACAACAACGACGACGACGCCCCAGGCCCCAGCTCAAGGATCTGGAGGGGCCG 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521 TCGCCGCCCTCACCAACAGCATCGGCGTCCTCGGCGTCGCCCCGAGCGCC---AGCCTCT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638 rogadreseccarceccaacaacarssacercarcarcarsacerceseccesses 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon-optimized RAmy3D signal-prosubtilisin BPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.3%; Score 50.8; DB 3; Length 1 Best Local Similarity 52.3%; Pred. No. 0.018; Matches 137; Conservative 0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear STREBT: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                       0665-0007.30
JMBER: US/09/023,173
13-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/038,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1593 TCGGCGCCGAGGACGACAC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            758 CCCCCCCCCCAACGAGGCAC 779
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                                                                                                                    FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: P42995
                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1140 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                        TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                           FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: line
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US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227 GGTATACTTCATATAAATCATATTAAGGATAAATGTATTTTATTAAAATATTACATGAAC 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633 ATTCGGTAATGGAACTAGAGTATTTGTTTTATTAATTGGACCTTTATGAAATACTAGTAG 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 AAITCAACGAAACTACAITCITCITTATIGGITATATIAGTAGTAATITGCITCACTAGA 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 AUTHAUTUTATIAGACUTGATICGICATCAAATATUTUTAAGCATGACATAAACATTT 991
                                                                                                                                                                                                                                                                                                            513 TCTAGCATTACTCATATTCACATATATATATATATGATAATATTCTAGATTCATTATCAT 572
                                                                                                                                                                                                                                                                                                                                                           929 ATATATATATTTTTTAAATATTTTAAAAGAGAAAAGAATGAAAAATGTACATATGTA 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  872 CGTTCACTTTTGTCCAACGTTTGACCATTCGTCTTATTAAAAAAATTATGTATCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           753 AITCTATITIAIACTAGAGAGITIAAAAATTATTACAAAACTAACTGTATACCGITGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    813 ACGGAATAGTAATATGGACCTATTACTTATTACTACCTCCATATTTTAATG-TATGACGC
                                                                                                                                                                                                                  Score 51.2; DB 4; Length 6124;
Pred. No. 0.031;
0; Mismatches 268; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09023173
Patent No. 6066781
GENERAL INFORMATION:
APPLICANT: Sutliff, Thomas D.
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION:
TITLE OF INVENTION:
IN Plants
TITLE OF INVENTION:
IN Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          992 TCATATTTGCAAAAAAAAAAAGGAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1347 TTGTTAATATAAGAATAAATAAAAA 1372
                                                                                                                                                                                                           2.3%;
al Similarity 46.4%;
235; Conservation
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MEDIUM TYPE: Diskett
                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (3850)..(5835)
US-08-213-419B-3
(2407)..(2439)
                                               (2598)..(3404)
                                                                                              (3580)..(3720)
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US-09-023-173-4
                                                                       NAME/KEY:
LOCATION:
    LOCATION:
                           NAME/KEY:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               596 GAAAATCTTATAACCTGAAACAGGGAGTATATATAATTCGGTAATGGAACTAGAGTAT 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 INGITITATTATTAGACCITTATGAAATACTAGTAGAATTCAACGAAACTACATTCTTC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716 TITATINGGITATATTAGTAGTAATTIGCTICACTAGAATTCTATTTTATACT - AGAGAG 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 ATTABABATTATTACAAAACTAACTGTATACCCGTTGCAACGGAATAGTAATATGGACCT 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      894 TGACCATTCGTCTTATTAAAAAAATTATGTATCTATTATTATTATTATTATTATTATTATGACTTGAT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 ITCCCIGGAATITCCTTCGTTTCATATTATAAGGTTTTCTAGCATTACTCATATTCACAT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           834 ATTACTTATTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Score 50.6; DB 2; Length 19124; 44.8%; Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 954 TCGTCATCAAATATTTTTAAGCATGACATAAACATTTTCATATTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 289; Indels
SOFTWARE: PatentIn Release #1.0, Version #1.25
              CURRENT APPLICATION DATA:

**PELICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSON, Ned
REGISTRATION NUMBER: 29,655
REFERRONCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
SEQUENCE CRRAACTERSTICS:
SEQUENCE CRRAACTERSTICS:
                                                                                                                                                                                                                                                                                                                         LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.35
Best Local Similarity 44.85
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

MANT-SENSE: NO

US-08-487-826B-13
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Search completed: March 26, 2003, 13:11:56 Job time : 246.441 secs

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March 26, 2003, 05:23:30 ; Search time 121.358 Seconds
(without alignments)
15433.627 Million cell updates/sec
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2201
1 cgtcgttcgttttgtgcatc......tagcttgtgctttgctgta 2201
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                   574371 seqs, 425486471 residues
                                                                                     - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                    IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
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                                                                                   OM nucleic
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                                                                                                                               Run on:
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Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/USC1_PUBCOMB.seq:*

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4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

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7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* 10: 11: 12: 13: Database :

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	g Query Match	* Query Match Length DB	DB	ID	Description
-	143.6	6.5	2000	10	US-09-887-576-859	Sequence 859, App
7	124.4	5.7	356	10	US-09-770-791-606	
m	110.2	5.0	689	10	US-09-770-149-308	
4	100	4,5	33675	10	US-09-921-992-2	Sequence 2, Appli
5	97.4	4.4	2000	10	US-09-887-576-832	832
ø	96.6	4.4	2000	10	US-09-887-576-859	Sequence 859, App
7	, 92.8	4.2	2000	10	US-09-887-576-862	Sequence 862, App
œ	72.6	3.3	33675	10	US-09-921-992-2	Sequence 2, Appli
σ	72.4	3.3	2000	10	US-09-887-576-832	Sequence 832, App
10	59.6	2.7	550	10	US-09-791-171-63	
11	56.6	2.6	390	10	US-09-790-399-7	
12	53.4	2.4	2000	Φ	US-09-938-842A-4849	Sequence 4849, Ap
13	51.6	2.3	2520	თ	US-09-858-525A-9	Sequence 9, Appli
14	51.4	2.3	640681	10	US-09-790-988-1	Sequence 1, Appli
15	49.2	2.2	4880	6	US-09-927-827-35	Sequence 35, Appl
16	49	2.2	2000	6	US-09-938-842A-3436	Sequence 3436, Ap
17	48.8	2.3	516	10	US-09-960-352-5785	Sequence 5785, Ap
18	48.8	2.5	3624	10	US-09-927-112-3	Sequence 3, Appli
13	48.8	2.2	4635	10	US-09-927-112-1	Sequence 1, Appli

Sequence 5558, Ap Sequence 4225, Ap Sequence 1100, Ap Sequence 40, Appl Sequence 40, Appl Sequence 1211, Ap Sequence 1211, Ap Sequence 121, Appl Sequence 134, Appl Sequence 124, Appl Sequence 124, Appl Sequence 124, Appl Sequence 1284, Appl Sequence 1284, Appl Sequence 1212, Ap Sequence 1212, Ap Sequence 1212, Ap Sequence 1212, Ap Sequence 1312, Appl Sequence 332, Appl Sequence 332, Appl Sequence 346, Appl Sequence 68, Appl Sequence 724, Appl Sequence 724		t expression Length 2000; Indels 10; Gaps 3; GAGGGGTGACTT 811 AAGGAGTTGACTT 1533	ח ת
US-09-960-3752-558 US-09-938-842A-4225 US-09-938-842A-3641 US-09-969-373-1100 US-09-961-373-1100 US-09-961-373-1100 US-09-861-28940 US-09-861-28940 US-09-864-761-22317 US-09-388-462-14 US-09-388-462-14 US-09-388-462-14 US-09-988-462-4 US-09-174-853-4 US-09-174-853-4 US-09-174-853-4 US-09-174-853-4 US-09-174-853-4 US-09-174-863-33-4 US-09-174-864-346 US-09-174-864-346 US-09-174-864-346 US-09-174-864-346 US-09-174-864-346 US-09-174-864-346 US-09-174-864-346 US-09-174-864-346	ALIGNMENTS	regulation of plant 7887,576 13,848 14,087 58,692 sion 4.0 OCTCAPATITAANGTANG FILE	IIIICCACCIIIGACCAILCGICIATIAAAAAAAA TAAGGAACAALTAATAATTAATTAATAAAAAAAATTTAATAAAAAAAA
2.2 431 10 2.2 1729 9 2.2 2008 310 2.2 2087 9 2.2 2787 10 2.2 2787 10 2.2 3787 10 2.2 3786 9 2.2 3786 9 2.1 3468 9 2.1 475 10 2.1 1850 9 2.1 51350 9		RESULT 1 US-09-887-576-859/C Sequence 859, Application US/09887; Parent No. USZOD0144047A1 GENERAL INFORMATION: APPLICANT: Budworth, P. APPLICANT: Budworth, P. APPLICANT: Chang, H. APPLICANT: Chang, H. APPLICANT: Han, B. APPLICANT: Wang, X. APPLICANT: Cooper, Bret TITLE OF INVENTION: DOINGER: US/09, CURRENT APPLICATION NUMBER: US 60/23 PRIOR PILING DATE: 2001-06-23 PRIOR PILING DATE: 2000-06-23 PRIOR PILING DATE: 2000-06-23 PRIOR FILING DATE: 2000-06-23 PRIOR FILING DATE: 2000-06-23 PRIOR FILING DATE: 2000-12-29 PRIOR FILING DATE: 2000-06-23 PRIOR FILING DATE: 2000-06-3 PRIOR FILING DATE: 2000-12-29 COFTWARE: PESEQ for Windows Ver. CORGANISM: Oryza sativa US-09-887-576-859 GUETY MATCH BEST LOCAL SIMILARITY 79:88; Pr. MATCHES 210; CONSERVATIVE 0; MATCHES 210; CONSERVATIVE 0; MATCHES 210; CONSERVATIVE 0; MATCHES 210; CONSERVATIVE 0; MATCHES 210; CONSERVATIVE OF 0; MATCHES 210	AACGIIIGACCTITCG
22222222222222222222222222222222222222		SULT 1 -09-887-576-859/C Sequence 859, Application Partent No. US20020144047A1 APPLICANT: Budworth, P. APPLICANT: Butworth, P. APPLICANT: Envon, D. APPLICANT: Chang, H. APPLICANT: APPLICANT: Promo TITLE FOR INVENTION: Promo TITLE FOR INVENTION: DAM APPLICANT: Wang, X. APPLICANT: Wang, X. APPLICANT: Wang, X. APPLICANT: APPLICATION NUMBER: PRIOR APPLICATION NUMBER: DRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0 PRIOR FILING DATE: 2000-0 PRIOR PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-1 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-1 PRIOR FILING DATE: 2000-1 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-1 PRIOR FILING DATE:	3.2
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                                 1472 TTATTGTGACTTGATTTATCATCAAATGTTCTTTAAGCATGATATAAGTATTTTTGTATT 1413
                                                                  999 IGCAAAAAAAA-----AAAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCA 1051
                                                                                     1412 FGCATAAAAATTTGAATAAGACGAATGGTCAAACGTTGGTTAAAAAGCTGTCA 1353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Horban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
PRIOR APPLICATION NUMBER: 60/118,480
PRIOR FILING DATE: 2000-01-07-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 606
                                                                                                                                                      1352 TACATTAAAATATGGAGGGAGTAT 1329
                                                                                                                                 1052 TACATTAAAATACGGAGGGATTAT 1075
                                                                                                                                                                                                                                                    Sequence 606, Application US/09770791
Patent No. US20020062014A1
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
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; ORGANISM: Arabidopsis thaliana
US-09-770-791-606
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Hamilton, Carol M.
Price, Jennifer L.
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Rameaka, Joshua G.
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Slader, Ted
Davis, Keith R.
Allen, Keith
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APPLICANT: Gorlach, Jorn
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1214 GAGAAGGIGAAGGAGCACATCGAGGAGAAGGCGGGGAGAGCAGTGGCGAAGCAACAACAAG 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: thaliana FILE REFERENCE: 2024 (PARA-013PKV)
CURRENT APPLICATION NUMBER: US/09/770,149.
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQUID NOS: 999
SOFTWARE: FASELSEQ for Windows Version 4.0
US/09770149
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OTHER INFORMATION: n = A,T,C or G
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
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ORGANISM: Arabidopsis thaliana
                                                                                              An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Rameaka, Joshua G.
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Hoffman, Neil
Hurban, Patrick
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Best Local Similarity 62.2
Matches 163; Conservative
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Davis, Keith R.
                                                                     Gorlach, Jorn
  Sequence 308, Application Patent No. US20020059663A1
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LOCATION: (1)...(689)
                                                 GENERAL INFORMATION:
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US-09-887-576-859
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LOCATION: (6224)...(7019), (7163)...(7269), (7344)...(7444), (7525)...(7634)
LOCATION: (7694)...(7813), (7923)...(8125)...(8253)...(8125)...(8125)...(8125)...(8125)...(8125)...(8125)...(8125)...(8125)...(8125)...(8125)...(8125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9125)...(9
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Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Zhu, B.
APPLICANT: And, B.
APPLICANT: And, B.
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Venkatramesh, Mylavarapu
TITLE OF INVENTION: Methyl-D-Erythritol Phosphate Pathway (
FILE REPERENCE: 16516.10/735-21(51897)US
CURRENT APPLICATION NUMBER: US/09/921,992
CURRENT FILING DATE: 2001-08-06
PRIOR PELING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTION: (1...33675)
COTHER INFORMATION: unsure at all n locations US-09-921-992-2
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                                                                                                                                                                                                         Rodriguez-Concepcion, Manuel;
Rohmer, Michel;
                                                                                                                                                                                                                                                                                        Seeman, Myriam;
Valentin, Henry E.;
Venkatesh, Tyamagondlu V.;
Sequence 2, Application US/09921992
Patent No. US20020069426A1
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                                                                                                                                                                           Campos, Narciso;
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                                                                          GENERAL INFORMATION:
APPLICANT: Boronat, Albert,
APPLICANT: Campos, Narciso
APPLICANT: Rodriguez-Conce
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ORGANISM: Oryza sativa
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US-09-887-576-832/c
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1662 TICIATCATITGATICATIATIAAATATATATITTICCGTATATATATATATITCATATITC 1603
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APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2000;
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CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 859
LENGTH: 2000
FILE REFERENCE: 1360.0010S1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR PPLICATION NUMBER: US 60/214,087
PRIOR PILIATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
NUMBER OF SED ID NOS: 875
SOFTWARE: FASLED for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Oryza sativa
US-09-887-576-832
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US-09-887-576-859
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4.4%; Score 96.6; DB 10; Length 2000;

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|1327 AT 1328
                       1076 AT 1077
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Matches 145;
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                                                                                                                                                                    1381 IGACCATICGICITATICAAAITITITATGCAAATACAAAATACITATATCATGCITAA 1440
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                                                                                                                                894 TGACCATTCGICTTATTAAAAAATTATGTAICT-----ATTATTTATTATTATGAC 948
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APPLICANT: Brown, D.

APPLICANT: Brown, D.

APPLICANT: Chu, T.

APPLICANT: APPLICANT: Brown, E.

APPLICANT: Han, B.

APPLICANT: MANGE, X.

APPLICANT: APPLICATION TOWNER: US 0.09/887,576

CURRENT APPLICATION NUMBER: US 0.02106.25

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 0.0214,087

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 0.0214,087
                                                                                                                                                                                                         949 ITGATICGICATCAAATATITITTAAGCATGACATAAACATTTTCATATTGCAA----
                     10;
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                     Indels
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 Pred. No. 8.4e-13;
0; Mismatches 74;
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67.4%; Pred. No. 6.8e-12;
iive 0; Mismatches 72
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PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SCHTWARE: FRASLSEQ for Windows Version 4.0
SEQ ID NO 862
LENGTH: 2000
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; Patent No. US20020144047A1
67.1%;
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Best Local Similarity 67.4
Matches 163; Conservative
                 171; Conservative
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US-09-887-576-862
 Similarity
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 Best Local
Matches 17
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16640 ARCITATITCAAAATITITIGIGAAATATAAAAACTATATGITATACATAAAGTATAIT 16699
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LOCATION: (7694)..(7813).(7923)..(8153),(8253)..(8369),(8515)..(8518)..
LOCATION: (9012)..(9071),(9163)..(9225),(9328)..(9472),(9589)..(9730),
LOCATION: (9951)..(1028)..(1028)..(10293),(10694)..(10798),
                                                                                                                                                                                   APPLICANT: Rodrigues—Concepcion, Manuel;
APPLICANT: Rodrigues—Concepcion, Manuel;
APPLICANT: Seeman, Michel;
APPLICANT: Seeman, Myriam;
APPLICANT: Valentin, Henry E.;
APPLICANT: Venkatesh, Tyamagoddlu V.;
APPLICANT: Venkatesh, Tyamagoddlu V.;
APPLICANT: Venkatemesh, Mylavarapu
TITLE OF INVENTION: Methyl-D-Erythritol Phosphate Pathway Genes
FILE REPERRANCE: 16516.107/35-21(51897)US
CURRENT APPLICATION UNMERR: US/09/921,992
CURRENT FILING DATE: 2001-08-06
PRIOR FILING DATE: 2000-08-07
WUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%; Score 72.6; DB 10; Length 33675; Similarity 59.2%; Pred. No. 3.3e-06; Conservative 0; Mismatches 94; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1.33675)
COTHER INFORMATION: unsure at all n locations 05-09-221-922-2
                                                                                                                                                                   Campos, Narciso;
Rodriguez-Concepcion, Manuel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 832, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
US-09-921-992-2
; Sequence 2, Application US/09921992
; Patent No. US20020069426a1
                                                                                                                                 APPLICANT: Boronat, Albert;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Oryza sativa
                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16820 TGAGA 16824
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TYPE: DNA
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APPLICANT: RASMISSEN, Peter Birk
APPLICANT: RASMISSEN, Ida
APPLICANT: RELDINGH, Karin
APPLICANT: FIORON, Malter
TITLE OF INVENTION: DERIVED FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: UCLETC ACIDS FRAGMENTS
TITLE OF INVENTION: UCLETC ACIDS FRAGMENTS
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
                                                                                                APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REPERENCE: 1360.001051
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3%; Score 72.4; DB 10; Length 2000; 58.3%; Pred. No. 5.1e-07; Live 0; Mismatches 101; Indels 5;
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-12-29
PRIOR PILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR PLINE DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR REPLING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
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US-09-887-576-832
Brown, D.
Chang, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                   Wang, X.
                                          Zhu, T.
Han, B.
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                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 832
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                   APPLICANT:
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  APPLICANT:
                                                              APPLICANT
                                          APPLICANT
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# Parent No. USZOUZUUSBUUUALI

# GENERAL INFORMATION:
# APPLICANT: Gold, Larry
# APPLICANT: Tuerk, Craig
# APPLICANT: Pribnow, David
# APPLICANT: Pribnow, David
# APPLICANT: Pribnow, David
# APPLICANT: Smith, Jonathan D.
# TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
# TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
# TITLE OF INVENTION Systematic Polypeptide Evolution by Reverse Translation
# TITLE OF INVENTION NUMBER: US/09/790,399
# CURRENT FILING DATE: 1998-11-23
# PRIOR FILING DATE: 1998-11-23
# PRIOR PLICATION NUMBER: 07/739,055
# PRIOR PLICATION NUMBER: 07/730,055
# PRIOR FILING DATE: 1991-08-01
# PRIOR FILING DATE: 1990-08-01
# PRIOR FILING DATE: 1990-08-01
# PRIOR FILING DATE: 1900-08-01
# PRIOR FILING DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 CGGCGACAAGAACAACGCGCGTCATCAAGGTGGTCCGGGAGATCGTTTCCGGCCTGGGCCT 369
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51.0%; Pred. No. 0.00096;
tive 0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 63
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ORGANISM: Artificial Sequence
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Best Local Similarity 51.0 Matches 134; Conservative
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Matches 146; Conserv
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1326 GAGGTCCCAAGATTTGCAGGTGCGAGATCACTCTTCACCAAGCGCCACGGCGTCATCC 1385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 ACACCCTCGTGGACCAGAAGCACCAGGAGTACCACTCCGTTCCGCTGGATCGGCCTGATCC 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRATURE: OTHER INFORMATION: modified DNA encoding ISPlA protein
                                                                                                                                                                                                                                                                                                                             APPLICANT: BOETS, Annemie
APPLICANT: ARMAUT, Greta
APPLICANT: ARMAUT, Greta
APPLICANT: AVAN RIE, Jeroen
TITLE OF INVENTION: No. US20020199215Alel Toxins
FILE REFERENCE: 021565-07
CURRENT APPLICATION NUMBER: US/09/858,525A
CURRENT FILING DATE: 2001-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/573,872
PRIOR FILING DATE: 2000-05-18
NUMBER. OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                       Sequence 9, Application US/09858525A Publication No. US20020199215A1 GENERAL INFORMATION:
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                                                                                                                               1569 AATTTAATACGATTTAAATAA 1549
                                                                             ACATITICATATITICCAAAAA 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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; LOCATION: (3)..(2510)
US-09-858-525A-9
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US-09-858-525A-9
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US-09-790-988-1
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wrong, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                     1432 CTCCTCCATCAAGAGGAAGCTCAGGAAGATCAAGGAGAAGAAGGAGACCGACGTCCGCCA 1491
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                                                                                                                                                                                                       1492 CCTCAAGGGGACCAAGCCCCCCGTCTCCGACTGGCCGCCATCATTGCTCGACAACAACGA 1551
1372 CCACGGCGTCATCCGCGCGGAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGC 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 CTAGTAGAATTCAACGAAACTACATTCTTCTTTATTGGTTATATTAGTAGTAATTTGCTT 745
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                               626 ATATATARTICGGTAATGGAACTAGAGTATTIGITTTTATTAATTGGACCTTTATGAAATA 685
                                                                                                                                                                                                                                                                                                                                                       806 CGTTGCAACGGAATAGTAATATGGACCTATTACTTATTACTACTCCTCCATATTTAATGTA
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Pred. No. 0.018;
0; Mismatches 191;
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CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PLILNG DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR PLILNG DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-01-06-22

NUMBER: OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4849, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                          1612 CACGGTGCTCACCAAGGTCTGCA 1634
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Best Local Similarity.
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US-09-938-842A-4849/C
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Publication No. US20030036176A1
GENERAL INFORMATION:
APPLICANT: Remseier, Thomas M.
TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris FILE REFERENCE: 88-10(15824)8
CURRENT APPLICATION NUMBER: US/09/927,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353121 TTTATAAATATAAAAAAATAAAGAATTAATCTTATAAACAGAATTATCATATTTTTTCTA 353180
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                                                                                                                                                                                                                                                                                                                                                                                 Length 640681;
                                   APPLICANT: HATTORI, MASABIRA
APPLICANT: HATTORI, MASABIRA
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
FURENY PELLOATION NUMBER: 108/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET: 2.1
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Pred. No. 3.1;
0; Mismatches 306;
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ilarity 45.5%;
Conservative
                      WATANABE, HIDEMI
APPLICANT: SHIGENOBU, SHUJI
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US-09-790-988-1
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LENGTH: 640681
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Best Local Simi
Matches 260;
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US-09-927-827-35
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/279,493
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 35
LENGTH: 4880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: March 26, 2003, 14:08:19 Job time: 1288.36 secs
                                                                                                                                                                        TYPE: DNA ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (1001)..(3880)
US-09-927-827-35
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Nucleotide sequenc Epstein Barr virus EBV tethering prot Nucleotide sequenc

Maize gibberellic Rice gibberellin Rice gibberellin

AAZ99478 AAH46558 AAH46555 AAV55831

AAA50254 AAF82902 AAA75454

AA164275

AAX90923

811 1187 1799 1799 1799 1926 2580 2580 2580 2580 10380 10380 10596 10596 10596 1181 1181

Anti-sense strand Vector pShuttle DN Vector plasmid pCM

> AAV21683 AAZ22248 AAQ51731 AAT40348

Epstein-Barr virus

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                                                March 25, 2003, 18:27:39 ; Search time 381.22 Seconds
(without alignments)
14774.266 Million cell updates/sec
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     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                 US-09-702-134-7212_COPY_28000_30500
2501
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Maximum Match 1100%
Listing first 45 summaries
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Match
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Perfect score:
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Human colon cancer FigA insert stabil Rice gibberellin 3 Genomic clone GlF MiSP1-containing p Wheat flavonol syn

> AA46557 AAQ55750 AAQ98470 ABL59991 AAC33593

Human immune/haema Genomic DNA encodi Human adenosine Al Corn tassel-derive

AAX53491 ABL75810 ABA50433

AAX04613 AAX04614 Human breast cell

ALIGNMENTS

Gibberelllin-20-ox RT-PCR product of Genomic sequence e

Arabidopsis thalia

Nucleotide sequent Plasmid pcisEBOM f Plasmid pcisEBOM i Nucleotide sequenc DNA clone pcEK Cl. Banana ethylene-fo DNA encoding ethyl Human genome from Epstein Barr Virus

AAX27502

AAX15650

AASO9902 AAD08215 AAX90924 AAK72613

AAA53800

AAA02484

1925 8298 77720 1000 1948 1505 2744 672

Arabidopsis thalia Arabidopsis thalia Gibberellin-20-ox Citrullus lanatus Gibberellin-20-ox CDNA encoding a C-Rice gibberellin 3 Soybean C-20 oxida

AAQ75360 AAD16847 AAC42398 AAQ75361 AAQ75361 AAQ75369 AAZ99483 AAZ99483

16 22 22 23 22 22 22 23

1259 1259 1169 1420 1395 1161 1122

292.4 292.4 290.8 271 229.6 228 226.4 153.2

2 2 4 5 6 7 8 9

Gibberelllin-20-ox

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TICCICIGCCCGGAGAIGGACACGCTGCTGCCCCCGCCGGAGGAGCTGGTCGACGACCAC 1718
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growth rate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 TCCACCAAGCTTCCATGGAAGGAGACCTTTCTTTCCGGT-----TTTGCGACGAC 494
                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGGCGCTG 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 gaggccreraagaagcacggrrrcrrcrcgregrcaarcacgcarcagcgaggrr 323
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                       clone pAt2301 containing DNA encoding gibberellin-20-oxidase may be used to construct chimeric genes and binary vectors to transform plants by usual methods, e.g. Agrobacterlum-mediated transfer. Propagated transgenic plants show modulated growth and development e.g. reducing GA-20-oxidase expression with antisense constructs reduces vegetative growth in cereals and grasses, improving resistance to frost, etc. Sense constructs improve fruit set and growth, extended stems and leaves, induce flowering and overcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495 ATGAGCCGCTCAAAATCCGTTCAAGATTACTTCTGCGATGCGTTGGGACATGGGTTTCAG
                                                                                                                                                                                                                                                                                         Preferred transgenic plants are maize and wheat.
                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 1259;
                                              New DNA encoding gibberellin 20-oxidase and related vectors - also host cells and transgenic plants, used to modulate plant growth and development, e.g. anti:sense constructs will reduce
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                       Sequence 1259 BP; 368 A; 304 C; 246 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                    Score 292.4; DB 16;
Pred. No. 1.2e-48;
0; Mismatches 336;
                                                                                                                            Claim 9; Page 75-76; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                    11.7%;
nilarity 60.0%;
Conservative 0
WPI; 1995-022813/03.
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 532; Conserv
                                                                                               regetative growth.
                 P-PSDB; AAR64143.
                                                                                                                                                                                                                                                                                         dormancy, etc.
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exhibiting at least one improved growth parameter, in that a DNA sequence coding for expression of a polypeptide exhibiting plant hormone gibberellin (GA) 20-oxidase activity functionally inserted in the plant genome. The transgenic plant is useful in forest, pulp and paper industries. The transgenic plant has increased growth rate, blomass production and/or xylem fiber length. The ectopic overexpression of GA 20-oxidase gene results in significant changes in growth rate, stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    volume and xylem fiber length, and thus reduces or eliminates the use of growth influencing chemicals in forestry. The present sequence is Arabidopsis thaliana gibberellin (GA) 20-oxidase CDNA construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a transgenic woody plant e.g. a Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic woody plant exhibiting improved growth parameter, useful in pulp and paper industries, comprises DNA sequence encoding gibberellin 20-oxidase activity functionally inserted in plant genome
                                                                                                   CACCCGAGGGTGTACCCGGACTTCACGTGGCGGGCGCTGCTGGACTTCACGCAGCGCCAC 1778
                                                                                                                                                   Transgenic plant, plant hormone, gibberellin, GA 20-oxidase, forest, pulp, paper industry; biomass production; xylem fibre length;
"Arabidopsis thaliana gibberellin (GA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana gibberellin (GA) 20-oxidase cDNA construct.
                                                                                                                                                                                                                                                                                           1779 TACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTA 1824
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12..1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 20; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD16847 standard; cDNA; 1259 BP.
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/product= "A1
20-oxidase"
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13-OCT-2000; 2000US-0240319.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
          Arabidopsis thaliana DNA fragment SEQ ID NO: 35404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0134221.
99US-0134370.
99US-0134768.
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99US-0139462.
99US-0139463.
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99US-0128234.
99US-0128714.
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99US-0130077.
99US-0130449.
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99US-0132485.
99US-0132486.
99US-0132487.
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99US-0134219
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                                                                                    Arabidopsis thaliana,
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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16 - JUN - 1999
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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23-APR-1999;
23-APR-1999;
                                                                                                            EP1033405-A2
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06-APR-1999;
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                                                                                                            999 CIGGAGGAGGCGCACCGGIGCAIGGACGCCTICITCACGCIGCCGCIGGGGGAGAAGCAG 1058
                                                                                                                                                                                                              GCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGGCTGGAGATGAA 1178
                                                                                                                                                                                                                                                              1179 GAGGGCGAGGAGGCCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGGCGGAGCACGGGCGG
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                                                                            264 GAGGCCIGTAAGAAGCACGGTTTCTTCCTCGTGGTCAATCACGGCATCAGCGAGGAGCTT 323
                                                                                                                              324 AIATCAGACGCICATGAATACACGAGCCCTTCTTTGATATGCCTCTCCCGAAAAACAG 383
                                                                                                                                                                                     384 AGGGTTCTTAGAAAATCCGGTGAGAGTGTTGGCTACGCAAGCAGTTTCACCGGACGCTTC 443
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                                                             939 GAGGCGTGCGAGGCACGCCTTCTTCTGCTGGTTAACCACGGCATCGAGGCGGCGCTG 998
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                                      Gaps
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          Score 292.4; DB 22; Length 1259;
Pred. No. 1.2e-48;
0; Mismatches 336; Indels 18;
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          11.7%;
60.0%;
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                                      Matches 532; Conservative
                       Similarity
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           Query Match
Best Local S
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990S-0143542.
990S-0144065.
990S-0144085.
990S-0144086.
990S-0144325.
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9905-0145088
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9905-0145195
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9905-0145218
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990S-0150566.
990S-0150884.
990S-0151065.
990S-0151066.
                                 99US-0140823.
99US-0140991.
99US-0141287.
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99US-0142055.
99US-0142390.
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99US-0144632.
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99US-0144814.
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99US-0149723.
99US-0149929.
99US-0149902.
       99US-0139899
99US-0140353
                   23-JUN-1999;
24-JUN-1999;
28-JUN-1999;
29-JUN-1999;
30-JUN-1999;
                                                     01-JUL-1999

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08-JUL-1999

12-JUL-1999

13-JUL-1999

14-JUL-1999
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20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
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2-JUL-1999;
2-JUL-1999;
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13-AUG-1999;
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16-AUG-1999;
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999 CTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGAGAAGCAG 1058
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Pred. No. 2.4e-48;
0; Mismatches 337; Indels
990S-0151080.
990S-0151303.
990S-0151303.
990S-0151930.
990S-015303.
990S-0153758.
990S-0154779.
990S-0155139.
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990'S-0156596.
990'S-0157117.
990'S-0157753.
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990S-0159295,
990S-0159330,
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99US-0159638.
99US-0159584.
99US-0160741.
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99US-0161404.
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990S-0161359.
990S-0161360.
990S-0161361.
990S-0161920.
990S-0161993.
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59.9%;
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99US-0158232
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Matches 531; Conservative
                                                                                                       23-SEP-1999;
24-SEP-1999;
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                                  ATGGAGGTGCTCGGGGAGAGCCTGGGCATCGTCGGAGACCGGCGCCCACTACTTCCGGCGA 1358
                                                                                          CICGACACGCIGGGCACCGGICCGCACTGCGACCCCACCTCGCTCACCATCCTCCACCAG 1478
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                                                                       750 GATCICACACIAGGAACAGGACCICATIGIGATCCAACAICITTACCAICCTICACCAA 809
                                           CCATTTGGGAAGGTGTATCAAGAGTATTGTGAAGCAATGAGTTCTCTATCACTGAAGATC
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                                                                                                                                                                                                                                                                                                                       Clone pAT2353 containing DNA encoding gibberellin-20-oxidase may be used to construct chimeric genes and binary vectors to transform plants by usual methods, e.g. Agrobacterium-mediated transfer. Propagated transgenic plants show modulated growth and development e.g. reducing GA-20-oxidase expression with antisense constructs reduces vegetative growth in cereals and grasses, improving resistance to frost, etc. Sense constructs improve fruit set and growth, extended steams and leaves, induce flowering and overcome dormancy, etc. Preferred transgenic plants are maize and wheat.
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                                                                                              New DNA encoding gibberellin 20-oxidase and related vectors -
also host cells and transgenic plants, used to modulate plant
growth and development, e.g. anti:sense constructs will reduce
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Pred. No. 2.2e-44;
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Best Local Similarity 56.5%;
Matches 593; Conservative
WPI; 1995-022813/03.
P-PSDB; AAR64144.
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                                                    CGGTCGTCAACAGCACGCGCCTCGCCGCTCGCTGGCCTTCTTCCTCTCCCGGAGATGG 1677
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GACCICATIGIGATCCAAGIICTTIGACCAICCTTCAICAAGACCAIGICAAIGGCCIIC 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to testa specific Cv20ox gene, a gibberellin 20-oxidase (GA 20-oxidase) gene which is integument-specifically expressed in seeds of the Citrullus lanatus, and proteins encoded by such genes. The invention also relates to Cv20ox promoter
                                                              Testa specific Cv20ox gene; gibberellin 20-oxidase; GA 20-oxidase;
Cv20ox promoter; Cv20oxP; seedless fruit generation; watermelon;
melon; ss.
                           AGGTGTGGGCGGAGGGCGCGCGCCCATCCGCCCTCGCCCCGGGGCGCGCTCGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCCTCCACCAGGACCACGTCGGCGGCCTGGAGGTGTGGGCGGGAGGGGCGGTGGCGCGC 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCCGCCTCGCCCCGGGGCGCTCGTCGTCAACGTCGGCGACACCTTCATGGCGCTCTC 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACGCCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCCG 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAATGGCCTTCTTTCTATGTCCAGCGGCTGACAAAGTGGTGAGAGCACCGGACGAAGT 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGGAGAAGAATCCACCAAGGAAGTTTCCAGATTACACATGGCCAATGCTGCTTGAACT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAA 1825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 TGATATGGAATTGATAAAAGGGGTTCATGAGTGTATGGATGTATTTCACATTGCCTTT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 TGATGTGAAACAAAATCTCAAAGGAAATTTGGTGAAAATTATGGGTATGCTAATAGCTT 467
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                               747 AIGCGAGAAGCCAGAGCTGACATTGGGAACTGGGCCTCACTGTGATCCAACCTCATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTGGAGATGAAGAGGGCGAGGAGGCCTTGGTGAGTACCTGGTGCGGAAGCTTCGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCGCTGGAGCTGAGGTGCTCGGGGAGAGCCTGGGCATCGTCGGAGACCGGCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1346 CTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAACTACTACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 --CITATGIIGCIAAICAIAAIICCACCICIGIICAGGAIIICGIIICIAAAIGIGIIIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCCAGAGGCCACTCGACACGCTGGGCACCGCACTGCGACCCCACCTCGCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTCTTCACCAAGACCACGTCGCCTTCAAGTCTACGTGGATGATGAGTGGCACTC
(Cv20oxP) which regulate the expression of Cv20ox gene and method for generating seedless fruits of gourd family such as melon or watermelon using the Cv20ox sequence. The present sequence is C. lanatus Cv20ox cDNA coding for GA 20-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATTGGAAGAITCTCCAATAATCTTCCATGGAAGGAAACCCTTTCCCTTC------
                                                                                                                                                                                                         DB 24; Length 1420;
                                                                                                                                            Sequence 1420 BP; 412 A; 257 C; 329 G; 422 T; 0 other;
                                                                                                                                                                                                                                 .7e-36;
es 384;
                                                                                                                                                                                                   9.2%; Score 229.6;
llarity 55.3%; Pred. No. 3.7e
Conservative 0; Mismatches
                                                                                                                                                                                                                                    Local Similarity
ses 501; Conserv
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1648 CGCTGGCCTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGCTGCCCCCCCGGAGGAGCTGG 1707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIGGAGAIGAAGAGGGCGAGGAGGGCGIGGGIGAGIACCIGGIGCGGAAGCICGGGGGGG 1227
                                                                                                                                                                                                                    1288 CGCTGGAGCTGATGGAGGTGCTCGGGGAGACCTGGGCATCGTCGGAGACCGGCGCCCACT 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                       1528 TCCGCCCTCGCCCCGGGCGCTCGTCGTCAACGTCGGCGACACCTTCATGGCGCTCTCCA 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase, C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1768 CGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAA 1825
                                                                                                                                                                        766 TCCTTCACCAAGACCCTGTCAGTGGCCTTCAAGTGTGCTCCAATGATCAATGGTATTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1588 ACGCCAGGTACCGCAGCTGCCTGCACCGGCCGGTCGTCAACACAGCACGGCGCCTCGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1108 CGGGGCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGACGCTGTCGTTCCGGTACTCATCGG
                                                                                                                                              1228 AGCACGGGCGGCGGCTGGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCTGT
                                                                                                                                                                                                                                            GCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACCTCGCTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   826 TTCCTCCAAACCCAGAAGCCTTTGTCATCAACATCGGTGACACTTTCACGTCTCTCACGA
                                                                                                           CICAAAACTCCICCGCGGGTCATGACTATGTTCTTGACACTTTAGGCCCATCATTCTCCC
                                                                                                                                                                                                                                                                                           ACTICCGGCGATICTICCAGCGCAACGACTCCATCATGCGCCTCAACTACTACCGGCGT
                                                                                                                                                                                                                                                                                                                            646 ACTICAAGAATTICTICGAGGACAACGATTCAATATTGAGGCITAATTACTACCAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding a C-20 oxidase polypeptide.
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/product= "C-20 oxidase"
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1..1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200009722-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vectors containing DNA encoding gibberellin-20-oxidase activity are used to construct chimeric genes and binary vectors to transform plants by usual methods, e.g. Agrobacterium-mediated transfer. Propagated transgenic plants show modulated growth and development e.g. reducing GA-20-oxidase expression with antisense constructs reduces vegetative growth in cereals and grasses, improving resistance to frost, etc. Sense constructs improve fruit set and growth, extended stems and leaves, induce flowering and overcome dormancy, etc. Preferred transgenic plants are maize and wheat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCAGGTGGGGAGGCGTGCGAGGCACGGCTTCTTCTTCTTGGTGGTTAACCACGCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA encoding gibberellin 20-oxidase and related vectors -
also host cells and transgenic plants, used to modulate plant
growth and development, e.g. anti:sense constructs will reduce
vegetative growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1395;
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                                                                                                                                                                                                                                          Gibberellin-20-oxidase; plasmid pB11; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 1395 BP; 404 A; 288 C; 336 G; 367 T; 0 other;
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Pred, No. 7.6e-36;
0; Mismatches 380;
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                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "GA-20-oxidase"
                                                                                         AAQ75359 standard; cDNA to mRNA; 1395
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 72-73; 97pp; English.
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                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                     Gibberelllin-20-oxidase
                                                                                                                                                                                                                                                             crop improvement; ss.
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Local Similarity
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 1167 AAAACA 1172
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                                                                                                                              AAQ75359;
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632 ACTICAAGAAITTCTICGAGGACAACGATTCAATATTGAGGCTTAATTACTACCCCAACAI 691
                            GCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCCACCTCGCTCACCA
                                                         GCGACAAGCCAGAGGTTGTGTTGGGAACTGGCCCTCACACTGATCCCACCTCGTCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsuoka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice gibberellin 3beta-hydroxylase cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 53-56; 68pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           new breeds of plants
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growth or
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                                                                                                                                                                                                                                                                                                                                                      a chimeric expression construct expressing a NNA or protein which suppresses the gibberallin biosynthetic pathway sequence, divarts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta, 3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to requilate gene products of gibberallin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberallin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1167
                                                                                                                                                                                                               Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           988 AGGCGCCCTGCTGCAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGG 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1048 GGGAGAAGCAGCGGGGGGGGGGGGGGGGGGAGCTGCGGCTACGCCAGCAGCTTCA 1107
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                                                                                                                               SJ;
                                                                                                                                                                                                                                                                                                  The present sequence encodes a C-20 oxidase polypeptide, which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels dibberellic acid levels may be inhibited or controlled by use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 GGCTGGTGGATGAGGCTTGTAGACAACATGGCATATTTTTTGTGGGGAACCATGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     928 GGCAGGTGGGGGAGGCGTGCGAGAGGCCACGGCTTCTTCCTGGTGGTTAACCACGGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 ATGTGAAGCAGAGGCTAAGAGGAAGGTAGGTGAGGTTATGGATATACCAATAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1108 CGGGGCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 TTGGGAGATTCGCGTCCAATCTTCCATGGAAGGAAACCTTTTCCCTTCGCTGTGTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1168 CTGGAGATGAAGAGGGGGGAGGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 CTCAAAACTCCTCCGCGCCTCATGACTATGTTCTTGACACTTTAGGCCCCATCATTCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------AAGGCGTATCAAGAGTGTGGGATAGCATTGAACGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 581 GTACGAAGATTGTGGGAGCTTTGGGGCTTAGCCTTGGCATTTCAAGAG------AAT
                                                                                                                              Logusch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                            Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1161 BP; 307 A; 251 C; 303 G; 300 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.5e-35
                                                                                                                            Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 226.4;
                                                                                                                                                                                                                                                                        Claim 45; Page 257; 267pp; English.
                                                                                                                           Heck GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.18;
                                                                                                                                           Ream JE;
                           99WO-US18066
                                                      98US-0096111
99US-0137977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 496; Conservative
                                                                                                                           Elich TD,
                                                                                                                                                                     WPI; 2000-224351/19.
                                                                                                (MONS ) MONSANTO CO.
                                                                                                                                           Rao S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                    P-PSDB; AAY84102
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                         10-AUG-1999;
                                                      10-AUG-1998;
07-JUN-1999;
24-FEB-2000
                                                                                                                     SM,
KJ,
                                                                                                                                                                                                              Obtaining
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                                                                                                                                           Piller
                                                                                                                              Brown
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Rice, gibberellin 3beta-hydroxylase, growth inhibition; gene expression; crop yield; plant breeding; plant regeneration; growth control; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to nucleic acid molecules from Oryza sativa that encode proteins with gibberellin 3beta-hydroxylase activity. The protein, the genes that encode them and antisense DNAs are useful for regulating gibberellin activation, e.g. to inhibit elongative growth or to improve crop yield and management. They are useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1588 ACGCCAGGTACCGCAGCTGCCTGCACGGGCGGTCGTCAACAGCACGCCGCCTCCGCCGCT 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGACGACCACCACCCGAGGGTGTACCCGGACTTCACGTGGCGGGGGCGCTGCTGGACTTCA 1767
TCCTCCACCAGGACCACGTCGGCGGCCTGGAGGTGTGGGCGGAGGGGCGGTGGCGCGCCA 1527
                                                                                                                                                                                                                             871
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                                                                    recriteaceaagaceergreggeerreaagrergercreaargarcaarggrarreaa 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            812 TICCICCAAACCCAGAAGCCTTTGTCATCAACATCGGTGACACTTTCACGTCTCTCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGGATTTACAAGGGCTGCATACACCGCGCTGTAGTGGAATTCCATGAATGCAAGAAAAT
                                                                                                                                                     TCGCCCCTCGCCCCGGGGGGCGCTCGTCGTCAACGTCGGCGACCTTCATGGCGCTCTCCA
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new breeds of plants, for producing a higher harvest of feeding materia for animals and in plant regeneration. They are used to control the growth, size and shape of plants, e.g. dwarf plants, by inhibiting the gene, expression. The present sequence encodes a rice gibberellin 3beta-hydroxylase enzyme of the invention.
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                                                                                                                                                                                  GCGGGCAGACGGAGATCCCGTCGCAGTTCATATGGCCGGCGGAGGAGAGCCCCGGGTCGG
                                                                                                                                                                                                             47 GGGCGGCGAGGCGGGTGCCGGACACGCACGCGTGGCCTGGACGACCACCCGGTGG
                                                                                                                                                                                                                                                                                                                       ACGGCATCGAGGCGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGC
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                                                                                                                                                      18;
                                                                                                                        Length 1122;
                                                                                                                                                      Indels
                                                                                          Sequence 1122 BP; 137 A; 406 C; 410 G; 169 T; 0 other;
                                                                                                                      Score 174; DB 22;
Pred. No. 3.9e-25;
0; Mismatches 495;
                                                                                                                      7.0%;
                                                                                                                                   Best Local Similarity 49.8 Matches 509; Conservative
                                                                                                                        Query Match
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The present sequence represents the C-20 oxidase polynucleotide sequence. In polynucleotide sequence is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be control of gibberellic acid levels. Gibberellic acid levels may be controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin the pathway. Or chosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copally diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have
                                                        1753 CGCTGCTGGACTTCACGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCT 1812
                                                                                           995 AGTACATGGCCGTCCGCAAGAAGGCCTTCGCCACGGCGCGCTCCGCCCTCAAGATGGTCT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obtaining transgenic plant useful for controlling seed germination an seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                        Gibberellič acid, copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-oxidase; 2beta, 3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
CGCTGCCGGAGGCCGTGCCGGCCGGCCGAGCCCCGCTACCGCGTGTCACGTGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 153.2; DB 21; Length 1077; Pred. No. 5.2e-21; 1; Mismatches 450; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hortened hypocotyl and/or epicotyl phenotypes compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 316 A; 219 C; 248 G; 288 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Logusch
                                                                                                                                                                                                                                                                                                                                                                         Soybean C-20 oxidase polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 45; Page 227-228; 267pp; English.
                                                                                                                                                                                                                                                              AAZ99421 standard; DNA; 1077 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ream JE;
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Best Local Similarity 50.1%;
Matches 470; Conservative
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07-JUN-1999;
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Gaps

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GCCACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAACTACTACC 1401
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                                                                                                                                                                                                                                                                                                                                                  GCTTCACGGGGCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACT 1161
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                                126 GCCCAAAGAGTICCTTIGGCCTTCTAGGGACTTGGTTGACACCACCCAAGAGGGAGCTAAA 185
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The present sequence represent a gibberellic acid 2-oxidase 2 cDNA sequence, which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthesic pathway sequence, diverts.

The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta, 3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to requilate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1274 GATGAGCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCATCGTCGC 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACTACCCGGCGTGCCAGAGGCCACTCGACACGCT---GGGCACCGGTCCGCACTGCGA 1450
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                                                                                                                                                                                                                                                                                                                                                                                             Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Obtaining transgenic plant useful for controlling seed germination ar seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
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                                                  Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytocone synthase; C-00 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin blosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
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                                                                                                                                                                                                                                                                                                                                                                                             Logusch EW,
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               Maize gibberellic acid 2-oxidase 2 cDNA sequence.
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Pred. No. 3.1e-16;
0; Mismatches 205
                                                                                                                                                                                                                                                                                                                                                                                           Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 45; Page 253; 267pp; English.
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Best Local Similarity 56.9%;
Matches 278; Conservative
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                                                                                                                                                                                  WO200009722-A2
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GGACGCCGCTGGGCCTCCGTCCCGCCCGACGGGGACGCCTTCTTCGTCAACGTCGGCGA 321

CDNA; 81:1

AAZ99478 standard;

AAZ99478 ID AAZ9 XX AAZ9 AC AAZ9 XX O3-J

(first entry)

03-JUL-2000 AAZ99478;

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Sequence 2112 BP; 462 A; 585 C; 576 G; 489 T; 0 other;
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Matches 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acid molecules from Oryza sativa that encode proteins with gibberellin 3beta-hydroxylase activity. The protein, the genes that encode them and antisense DNRs are useful for regulating gibberellin activation, e.g. to inhibit elongative growth or to improve crop yield and management. They are useful for producing new breeds of plants, for producing a higher harvest of feeding materials for animals and in plant regeneration. They are used to control the growth, size and shape of plants, e.g. dwarf plants, by inhibiting the gene expression. The present sequence is genomic DNA encoding a gibberellin 3beta-hydroxylase enzyme.
                                                                                                                                                                                                                                                                                                                                        Rice, gibberellin 3beta-hydroxylase, growth inhibition, gene expression, crop yield, plant breeding; plant regeneration; growth control; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice-originated gibberellin 3approximatelyb-hydroxylase and encoded quenes for regulating gibberellin activation e.g. to inhibit elongative growth or to improve crop yield and management, applicable to produce new breeds of plants
                                                                                                         GCGCCCGCCGGAGGAGCTGGTCGACGACCACCACCGGAGGGTGTACCCGGACTTCACGTG 1747
                                                         CAGCACGGCGCCTCGCCTCGCTGGCCTTCTTCCTCTGCCCGGAGATGGACACGGTGGT 1687
                                                                        Kobayashi M;
                                                                                                                                                                                                                                                                                                                  Rice gibberellin 3beta-hydroxylase genomic DNA #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 60-63; 68pp; Japanese.
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1..788
                                                                                                                                                                                                                                          AAH46558 standard; DNA; 2112 BP.
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789..899
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900..2112
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                                                                                1268 CCACGAGATGAGCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCAT 1327
                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                1439 TCCGCACTGCGACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGICAACGICGGCGACACCITCAIGGCGCTCTCCAACGCCAGGIACCGCAGCIGCCTGCA
                                         15;
    DB 22; Length 2112;
                                         Indels
Score 126.4; DB 22;
Pred. No. 1.3e-15;
0; Mismatches 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NORC ) JAPAN MIN AGRIC FORESTRY & FISHERIES (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice gibberellin 3beta-hydroxylase cDNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH46555 standard; cDNA; 1187 BP.
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    54.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001 (first entry)
                                           Conservative
                      Similarity
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GACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGGCCTGGAGGTG-
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                                                                                                                                                                                                                                                                                                                                                         AAV55831 standard;
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15-NOV-1996;
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                                                                                                                                                                                                                or to improve crop yield and management. They are useful for producing new breads of plants, for producing a higher harvest of feeding materials for animals and in plant regeneration. They are used to control the growth, size and shape of plants, e.g. dwarf plants, by inhibiting the apene expression. The present sequence encodes a rice gibberellin 3beta-hydroxylase enzyme of the invention.
                                                                        Rice-originated gibberellin Sapproximatelyb-hydroxylase and encoded genes for regulating gibberellin activation e.g. to inhibit elongative growth or to improve crop yield and management, applicable to produce
                                                                                                                                                             The invention relates to nucleic acid molecules from Oryza sativa that encode proteins with gibberellin 3beta-hydroxylase activity. The protein, the genes that encode them and antisense DNAs are useful for regulating gibberellin activation, e.g. to inhibit elongative growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      969 GTGGTTAACCACGGCATCGAGGCGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCC 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 TACACCTTCCCTCCCCTGCCATCCGCGACGAGTTCCGCCGCGCTCTGGCCCGACGCCGGC
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                                                                                                                                                                                                                                                                                                                                Score 114.8; DB 22; Length 1187; Pred. No. 2.3e-13;
                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                       Sequence 1187 BP; 202 A; 378 C; 424 G; 183 T; 0 other;
              Kobayashi
                                                                                                                                                                                                                                                                                                                                                         532;
                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
             Matsuoka M,
                                                                                                                                    Claim 1; Page 49-52; 68pp; Japanese.
             Yano M,
                                                                                                                                                                                                                                                                                                                                4.68;
                                                                                                                                                                                                                                                                                                                                                        Conservative
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E-
                                                                                                               new breeds of plants
                                     2001-418072/44
                                                                                                                                                                                                                                                                                                                                           Similarity
             Kayano
                                                 P-PSDB; AAG64062
                                                                                                                                                                                                                                                                                                                                                        466;
             H,
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Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                GTCAACAGCACGGCGCCTCGCCGCTCGCTGGCCTTCTTCTTCTTGCCCGGAGATGGACACG 1682
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                                                                                                                                                                                    858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be identical from n repeat to n repeat. Alternatively a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          919 GTGAACCGGGGGAGAGACCGGATCTCCTTCCTTCCTCGGTCCGCCGGCGGCGATG
CACCGGCCGGACCGGTGACGGTTCCGGGGACGCCGGGGGGCGCTCATCGTCGTCGTC
                                                                                                                                                                                                                                                                        GGCGATCTCTTCCATGTGCTCACCAACGGCGCTTCCACAGCGTGTTCCACCGCGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1683 GTGGTGCGCCCGCCGGAGGAGCTGGTCGACGACCACCACCGGAGGGTGTACCCGGACTTC
                                                                                                         TGGGCGGAGGGGCGCGCGCCCATCCGCCCTCGCCCCGGGGCGCTCGTCGTCAACGTC
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11-FEB-2000; 2000WO-US03547

(PHAR-) PHARMACOPEIA INC

11-FEB-1999;

Chelsky

Horlick RA,

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encoding the stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the unfused core protein. The products can be used for treating autoinmune diseases, cancer and inflammation. In particular, the core protein may be an Ikappa regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein which can activate nitro drugs in enzyme/produug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in diagnostic methods such as in vivo imaging.
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                                                                                                                                                                                 Score 94.4; DB 19; Length 799;
Pred. No. 2.3e-09;
0; Mismatches 256; Indels 0
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                                                                                                                                                        Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;
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                                                                                                                                                                                 3.8%;
ilarity 49.2%;
Conservative (
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                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                              248;
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                                                                                                                                                                                                                                                                                                                                               The present sequence is that of DNA encoding the Epstein-Barr virus (EBV) nuclear antigen protein 1 (EBNA1, see AAY95856). EBNA1 is utilised in a novel method for obtaining a eukaryotic cell that is stably transfected with at least one episome. This method involves transfecting a eukaryotic cell with: (1) a first episome comprising an EBV origin of replication (orip, see AAA50253), a gene encoding a first protein whose expression results in cell death and a
                                                                                                                                                                                                                                          Stably transfecting eukaryotic cells with at least one episome for production of a desired protein in vitro and for gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     First process marker for eukaryotic cells; and (2) a second episome comprising an EBV orip and a gene encoding a second protein, where expression of the second protein prohibits the occurrence of cell death resulting from expression of the first protein to produce doubly transfected cells which also express an antigen that promotes retention of the episomes by the cells. The doubly transfected cells are maintained under conditions in which the first and second proteins and the selectable marker are expressed, and the selective pressure specified by the marker is maintained. Under these conditions, only cells containing both episomes live. Preferably, EBNAl is expressed from 1 of the episomes, and the protein of interest from the other episome. Either or both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     establishment of exaryotic cells that stably and reliably express a gene of interest, using a novel method of selection, and maintenance of that selection without the need for exogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epitopes may further comprise a nucleic acid sequence encoding a protein desired to be expressed in the cell (e.g. a therapeutic protein), a nucleic acid encoding an RNA that is not intended to be translated (e.g. a therapeutic RNA), or a DNA sequence used as a tag for the cells. The method is applicable to cell culture or intest organisms, for gene therapy. It allows the rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         752 GGTGGTGCAGCAGCAGGAGGTGTGCTTCGACGCGGCGGTGCTGAGCGGGCAGACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         872 GCTGGAGGTGGCGCTGATCGACGTGGGGGCGGGGCGGAGAGGTCGTCGTGGTCCGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94.4; DB 21;
Pred. No. 2.9e-09;
0; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   selection factors, such as antibiotics.
                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 53pp; English.
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P-PSDB; AAY95856.
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protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral wector encodes a protein suitable for tethering DNA to Histone HI Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Epstein-barr virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8; EBV; latency-associated nuclear antigen; LANA; EBNA1; ds.
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                                                                                                              1112 GCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGGCTGC 1171
                                                                                                                                                                                                                                                   1172 AGAIGAAGAGGCGAGGAGGGCGIGGGIGAGIACCIGGIGCGGAAGCICGGGGCGGAGCA 1231
670 GCAGGAGGGCAGGAGGGGCAGGAGGGGGCAGGAGCAGGAGCAGGAGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EBV tethering protein EBNA1 encoding DNA.
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P-PSDB; AAB62332.
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                                                                                                                            932 GGTGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGC
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Length 1926;
                           Indels
3.8%; Score 94.4; DB 22;
49.2%; Pred. No. 2.9e-09;
tive 0; Mismatches 256;
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Job time: 417.887 secs
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Scoring table:

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BC7818 WHEZ153_G
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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    892 GCGCTCTCCAACGGGCGCTACAGGAGCTGCCTCCACGCGCCGTCGTCAACAGACCGGGTG 951
                                                                                                         1072 CTGGACTTCACCATGAGGCACTACAGGTCGGACATGAGGACGCTCGAGGCCTTCTCCCAAC
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Sequences have been tri
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                                                                                                                                                                           Pred. No. 1.1e-118;
0; Mismatches 241;
                                                                                                                                                              25.2%;
75.9%;
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                 Library
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les 825; Conserv
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1. 336
/organism="Sorghum bicolor"
/db_xref="taxmoi.4558" EM1)"
/clone_lib="mbryo 1 (EM1)"
/note="Organ: Embryo 3 germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
EcoKI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were
BG322884 536 bp mRNA linear EST 27-FEB-2001 EM__15_C10.bl_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
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                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences have been trimmed to exclude PolyA, vector and regions. below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1158 TACTCATCGGCTGGAGATGAAGAGGCGAGGAGGCCTGGGTGAGTACCTGGTGCGGAAG 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cordonier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
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                                                                                                                                                                                                                                                                                                                                                                           Pratt, L.H.
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                                                                                                                                                                                                                                                                                                                                                                        Gingle, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 286.8; DB 1
76.6%; Pred. No. 1.8e-48;
ive 0; Mismatches 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop:
POLYA=No.
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Anote—Worker lambdalab; Site_1: EcoR1; Site_2: Xhol; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 20 Dap (Fenton): Total RNA was prepared, poly(A) RNA was purified, one primary unamplified CDNA library was made, and 1 million pin were in vivo excised to give pBluescript SK(-) cDNA phagemids in the TJ Close lab at the University of California, Riverside (Choi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Pelmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence and wing). Plasmid DNA preparations, DNA sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library the paration and sequence mallysis seed that the contains a minimum of 100 bases of the paration and sequence mallysis seed that the contains a minimum of the contains a minimum of the contains that the contains the contains a minimum of 100 bases of the contains a minimum of the contains that the contains the contains the contains a minimum of the contains that the contains the contains the contains the contains the contains the contains a minimum of the contains the conta
tissue_type="20 DAP spike"
                                   /lab_host="SOLR"
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65.4%;
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1 (Dases 1 to 755)
Wing.R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 20 DAP spike cDNA library Unpublished (2001)

On Mar 8, 2001 this sequence version replaced gi:13254292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVSME10001L04f Hordeum vulgare 20 DAP spike EST library HYCDNA0010 (20 DAP) Hordeum vulgare CDNA clone HYSME10001L04f, mRNA sequence. BG365195.2 GI:16323591
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                 CTCGGGGCGGAGCACGGCGGCGGCGGGGGGGGGGTACTCGCGCTACTGCCACGAGATG 1277
                                                                                                                                 AGCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCCATCGTCGGAGAC 1337
                                                                                                                                                                                                                                              1338 CGGCGCCACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAACTAC 1397
                                                                                                                                                                                                                                                                                 TACCCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACC 1457
                                                       /db.rafe="taxon:4513"
/db.rafe="taxon:4513"
/clone="Hyski1001104f"
/clone=lib="Hordeum vulgare 20 DAP spike EST library
HVcDN4010 (20 DAP)"
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Seq primer: AATTAACCCTCACTAAAGGG
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Hordeum vulgare
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http://www.genome.clemson.edu/projects/barley. To order this close see http://www.genome.clemson.edu/corders Also see Close TJ. Wing R. Kleinhoffs A. Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 256 c 258 g 120 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  974 TAACCACGGCATCGAGGCGGCGGCTGCTGGAGGCGCGCACCGGTGCATGGACGCCTTCTT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1154 CCGGTACTCATCGGCTGGAGATGAAGAGGGGGGAGGAGGGCGTGGGGTGAGTACCTGGTGCG 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1394 CTACTACCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCC 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GAACCAGGGGTGGACCCGGCGCTGCTCGCCAAGGCGTACCGGTGCTGCCACGCCTTCTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CGCCGCCAGCTTCGTGGGGGGGGTTCGCCAGCAGCTCCCCTGGAAGAGAACATCTCTT 360
                                                                                                                                                                                                                                                                                                                                                                    797 GAGCGGGCAGACGGAGATCCCGTCGCAGTTCATATGGCCGGGGAGGAGAGGCCCCGGGTC 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGACGCGTGGAGGAGATCGTCCTGCTCGTCGTCGTCGTCCTGGCCGCGGT 120
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                                                                                                                                                                                                                                                      Length 755;
                                                                                                                                                                                                                                                                                                                231; Indels
                                                                                                                                                                                                                                                   Score 277.4; DB 12;
Pred. No. 1.4e-46;
0; Mismatches 231; 1
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Bordeum vulgare
Eukaryoch(st. Viridiplantae; Streptophyta; Embryochyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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BG299451
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  Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 257 c 257 g 127 t
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                                                                                                                                                                                                  22;
                                                                                                                                               Score 263.4; DB 12; Length 752;
Pred. No. 1e-43;
0; Mismatches 221; Indels 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 752)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
Ming, R., Close, T.J., Rleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
Y., Henry, D., Cates, R. and Main, D.
Development of a genefically and physically anchored BST resource
for barley genomics: Morex 20 DAP spike cDNA library
Unpublished (2001)
On Mar 8, 2001 this sequence version replaced gi:13254291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae, Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                               ar EST 22-OCT-2001
library HVcDNA0010
                                                                                                                                                                                                                                                                                                                                                    HVSME10001L03f Hordeum vulgare 20 DAP spike EST lbrary HVCDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10001L03f, mRNA sequence. BG365194
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                                                                            CACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGGCCTGGAGGTGTGGGCGGAGGG 1513
     /clone_lib="Hordeum vulgare 20 DAP spike EST library
HVCDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="Solk"
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                                                                                                                                                                                                                                                                                                                                                  mRNA
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100 Oordan Hall, Clemson, SC 29634, USA
THEL: 864 656 7288
Fax: 864 656 4293
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/cultivar="Morex"
/db_xref="taxon:4513"
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High quality sequence stop: 586.
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Total hq bases = 558
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaes; Mordeum.

1 (bases 1 to 577)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,Y.D., R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike CDNA library
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/clone="HVSMEh0086D02f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
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                                                                                              ACCACGGCATCGAGGCGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCA 1035
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On Jun 26, 2000 this sequence version replaced gi:13187496.
Contact: Wing RA
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Clemson University Genomics Institute clemson University 100 Jordan Hall, Clemson, SC 29634, USA Pax: 864 656 7288
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/cultivar≈"Morex"
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High quality sequence start: 21
High quality sequence stop: 543.
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Total hq bases = 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxine in covered crystallization dishes. Five-day old seedlings were incubated at Soc for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside
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1 (bases 1 to 796)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu.
Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W.,
Fenton,R.D. and Main,D.
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                                                                                                      resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0001 (Cold stress)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Darley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 272 c 247 g 146 t 24 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 811 AGAICCCGTCGCAGTTCATATGGCCGGCGGAGGAGAGCCCCGGGTCGGTGGCGGTGGAGG 870
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                                                                                                 Development of a genetically and physically anchored EST resfor barley genomics: Morex cold-stressed seedling shoot cDNA
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                                                                                                                                                                                               Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 644.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Total hq bases = 587
                                                                                                                                                                             Unpublished (2001)
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  REFERENCE
                               AUTHORS
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523 GAGGTGTTCACCGGCGCGCGCGTGGCGTGCCGTGCGGGCCCCGAGCGACGCCTTCG 577
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KEYWORDS
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                                                                                                                                                                                                                                                                                   SOURCE
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         요
                                                            Anote—Wetcor: lampda2AP; Site_1: EcoR1; Site_2: Xhol; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Clase, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Fotal RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give palbuscript SK(-) bonk phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics: Institute (CUG1) Regum. Palmer. Frisch, Akkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUG1 (Wing, TV, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or excession and experience and library preparation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1017 IGCAIGGACGCCIICTICACGCIGCCGCIGGGGGAGAAGCAGCGGGGCGCAGCGGCGCGCG
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(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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0; Mismatches 171; Indels 18;
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HVCDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
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Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly (A) RNA was purpared, poly (A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(·) cDNA phagemids. These steps were performed in the TJ close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemon Diversity enomics institute (CUGI) (Begum, Palmer, Filsch, Akkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were
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                             EST 22-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, Pooideae
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Wing,R., Close,T.J., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)
On Dec 18, 2000 this sequence version replaced gi:11884239.
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BF620505
HVSMEC0020B13f Hordeum vulgare seedling shoot EST library
HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEC0020B13f, mRNA sequence.
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HVcDNA0003 (Etiolated and unstressed)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/lab_host="TJC121"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 496.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HVSMEc0020B13f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
Total hq bases = 464
                                                                                                                                                                                                                         BF620505.2 GI:13109508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Triticeae; Hordeum.
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tests and pericarp were dissected from developing kernels at Washington State University, Pullman, WA (Kannangara, von Wetstein). Total RNA was prepared, poly(A) RNA was putified, one coRA library was made, and I million pfu were in vivo excised to give pBluescript SK(·) cDNA phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Phagemids mere plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Akkins and Wing). Plasmid DNA preparations, DNA sequence in Sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation, and sequence analysis see http://www.genome.clemson.edu/projects/parley. To order this clone see http://www.genome.clemson.edu/projects/parley. To order this clone see http://www.genome.clemson.edu/projects/parley. Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pww.usda.gov/ggpages/Dgu/31/cover.html)"
                                                                                                                                                                                                                                                                                               /tissue_type="testa/pericarp"
/lab_host="mydl21"
/note="vector: lambdazAP; Site_1: EcoR1; Site_2: Xho1;
Plants were raised from seeds in a Controlled Environments
growth chamber maintained in continuous light at 180c, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1411 AGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACCTCGCTCACCATCC 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1531 GCCCTCGCCCCGGGGCGCCTCGTCAACGTCGGCGACACCTTCATGGCGCTCTCCAACG 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1591 CCAGGTACCCCAGCTGCCTGCACCGGCCGGTCGTCAACAGCACGCGCGCCTCGCCGCTCGC 1650
                                                                                                                                                                                                                                                   /clone_lib="Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1471 TCCACCAGGACCACGTCGGCGCCTGGAGGTGTGGGCGGAGGGGCGGTGGCGCGCATCC 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1711 AC---GACCACCACCACGGGGGTGTACCCGGACTTCACGTGGCGGGGGGCGTGCTGGACTTCA 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1768 CGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAATC 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GGCCCCGGAGCGACGCCTTCGTCGACATCGGCGACACCTTCTCCGCGCTCACCAACG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 CCATTGATGGACGCCCCGCGCGTGTACCCCAGACTTCACTTGGCGTGAGTTCCTCGAGTTCA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 TCACCTICTICCTCAACCGCAGCTGGACGGCCCCGTCACGCCGCGGCCGAGCTGCTGCTGCTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AGAAGCCTCACCTGACGCTGGGCACGGCCCGCACGACGCCCGACGCCTGACGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GECGCCACGTCAGCTGCCTCCACGCGCCGTCGTCAACGGCAGCCTGGCCCGCAGGTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 213; DB 12;
Pred. No. 2.2e-33;
                                                                                                                                                   /organism="Hordeum vulgare"
                         Total hq bases = 618
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                            /clone="HVSMEk0013M18f"
                                                                                                                                                                                                  /db_xref="taxon:4513"
                                                                        High quality sequence stop: (
Location/Qualifiers
                                                                                                                                                                        /cultivar="Morex"
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Best Local Similarity
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ORIGIN
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Triticeae; Hordeum.

Triticeae; Hordeum.

To Close; T.J., Kleinhofs, A., Wise, R., Kannangara, G., von Wetstein, D., Akhunov, B., Chin, A., Choi, D.W., Fenton, R.D., Kianian, P., Otto, C., Simons, K., Zhang, D., Bequm, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simonns, J., Oates, R. and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Morex testa/pericarp cDNA library

Contact: Wing RA

Clease Indigersity Genomics Institute
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HVSMEk0013M18f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSNEk0013M18f, mRNA
                                                 ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               976 ACCACGGCATCGAGGCGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCA 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1216 AGCTCGGGGGGGGAGCACGGGCGGCGGCGGGGGGGGGTGTACTCGCGCGTACTGCCACGAGA 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 CCGAGGTGACCGCCTCGTCGCGAGGCCTGCGAGGGCCACGGCTTCTTCCAGGTCGTCA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 CCAGCAGCTTCACCGGCCGGTTCGCGTCCAAGCTGCCCTGGAAGGAGACCCTCTCCTTTC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 GGTCCTGCCCTTCGAA------CCCGGCCTCGTGGTGGACTACATTGTCGCCC 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         751 TGGTGGTGCAGCAGCAGCAGGAGGTGGTGCTTCGACGCGGCGGCGGTGCTGAGCGGGCAGACGG 810
                                                                                                                            918 TC--GGTGGTCCGCCAGGTGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTA 975
                                                                                                                                                                                               811 AGAICCCGICGCAGIICATAIGGCCGGCGGAGGAGAGCCCCGGGICGGTGGCGGIGGAGG 870
                                                                                                                                                                                                                                                                                                  --- GCCGGGGCGGAGAGGTCG 917
                                                   Gaps
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Length 914;
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DB 12;
                                                 0; Mismatches 156;
Score 230.4; DB 1
Pred. No. 5.7e-37;
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                               871 AGCIGGAGGIGGCGCTGATCGACGIGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG416635
BG416635.1 GI:13322186
9.2%;
                                                 Matches 404; Conservative
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                         Similarity
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Query Match
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VERSION
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AUTHORS
                                                                                                                                              129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369
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BG416635
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Gaps

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Length 682; Indels Ĥ

Gaps

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ESM Hordeum vulgaze

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Hordeum.

1 (bases 1 to 571)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu

K., Henry, D., Palmer, M., Rambo, T., Simcons, J., Choi, D.W., Fenton

, R.D., Close, S.J., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource

for barley genomics: Morex 5-45 DAP spike cDNA library

Unpublished (2001)

On Jul 26, 2000 this sequence version replaced gi:13189555.

Contact: Wing RA
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HVSNEh0095D08f Hordeum vulgare 5-45 DAP spike EST library
HYCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSNEh0095D08f,
mRNA sequence.
BE454826
BE454826.3 GI:16322121
                                                                                                                                                                                                                                   1411 AGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACCTCGCTCACCATCC 1470
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(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
186 c 161 g 98 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                  122 GGCCCGGAGCGACGCCTTCGTCGTCAACATCGGCGACACTTCTCGCGCGCTCACCAACG 181
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                                                                                                                                                                          3;
                                                                                                                    Length 566;
                                                                                                              Score 209.8; DB 12; Length
Pred. No. 1e-32;
0; Mismatches 122; Indels
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
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Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                                                 Query Match 8.4%;
Best Local Similarity 70.3%;
Matches 296; Conservative
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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Alabbast-"TJ2121"

Anote-"Vector: landaraPp; Site_1: EcoR1; Site_2: Xhol;

Anote-"Vector: landaraPp; Site_1: EcoR1; Site_2: Xhol;

Plants were raised from seeds in a Controlled Environments

growth chamber maintained in continuous light at 180c, and

testa and perioarp were dissected from developing Rernels

at Washington State University, Pullman, WA (Kannangara,

von Wetstein). Total RNA was prepared, poly(A) RNA was

purified, one cDNA library was made, and 1 million pfu

were in vivo excised to give pBluescript SK(-) cDNA

phagemids in the TJ Close lab at the University of

california, Riverside (Akhunov, Chin, Choi, Close, Fenton,

Kianian, Otto, Simons, Zhang). Phagemids were plated and

picked at the Clemson University Genomics Institute (CUGI)

(Begum, Palmer, Frisch, Aktins and Wing). Plasmid DNA

preparations, DNA sequence has been trimmed to remove

vector sequence and contains a minimum of 100 bases of

phred value 20 or above. For more details on library

preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum volgate:

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Hordeum.

1 (bases 1 to 566)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannangara, G., von

Wetstein, D., Akhunov, E., Chin, A., Choi, D. W., Frisch, D., Kianian

P., Otto, C., Simons, R., Zhang, D., Begum, D., Frisch, D., Yu, Y.,

Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource
for barley genomics: Morex testa, Pericarp cDNA library
                                                                                                                                                                                                                                BG414208 566 bp mRNA linear EST 23-OCT-2001
HVSMEK0001C12f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEK0001C12f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Hordeum vulgare testa/pericarp EST library HVcDNA0013 (normal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total hq bases = 168
Seq primer: AATTAACCTCACTRAAGGG
High quality sequence start: 9
High quality sequence stop: 545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEk0001C12f"
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1..566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                 BG414208
BG414208.1 GI:13319759
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Fax: 864 656 4293
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TITLE

SOURCE

FEATURES

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                    EST 25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outplitat="Wynna"

/db_xref="taxon:4565"
/clone_lib="wheat EST endosperm library"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
/days post anthesis)"
/note="Vector: Bluescript II SK(-)"

a 200 c 203 g 83 t i others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        943 CGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGGCGCTGCTGC 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1003 AGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGGAGAAGCAGCGGG 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1183 GCGAGGAGGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCGGGAGCACGGGCGGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 GCAAGCTCCCCTGGAAGGAGACCGTGTCCTTCAACTGCTCCGCCGGAGGGGGCCCC 465
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                                  567 bp mRNA linear EST 25-JUN PRNA linear EST 25-JUN PRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Plant Biology
                                                                                                                                                                                                                                                                                                                                                                                                genomic information
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Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 200; DB 14; Pred. No. 1e-30; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                   Clarke, B., Lambrecht, M. and Rhee, S. Assessing the utility of Arabidopsis interpreting wheat BST sequences Unpublished (2002) Contact: Lambrecht M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                         BQ606563.1 GI:21555890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.0%;
Best Local Similarity 66.7%;
Matches 354; Conservative
                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 567)
                                                                                                                                                                                                                                                   Triticum aestivum
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                                                                                                                                                                                                                      bread wheat,
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                                                                                                                                                                                                                                      Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified compared from the mixture, one primary unamplified or secised from the mixture, one primary in vivo excised to give pBluescript SK(-) CoMPA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the clemson University Genomics Institute (CUGI) (Regum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Midy, YY, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 202 c 190 g 87 t
                                                                                                                  /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
VrbonAc009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SolR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1072 GCGCGGGGGAGAGCTGCGGCTACGCCAGCTTCACGGGGCGCCTTCGCGTCCAAGCTGC 1131
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                                                                                                                                                                                                                      /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 CGGCGGAGGAGCCCCGGGTCGGTGGCGGTGGAGGTGGAGGTGGAGGTGGAGCTGATCGA-- 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTGTTCGACGCGGCGGTGCTGAGCGGGCAGACGGAGATCCCGTCGCAGTTCATATGGC 834
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F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 TCGCCGGGTTCCTGGCCGGCGACGACGCTGGCCTCAATGAGCTCGTCGCGGCGTGCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 GGCACGGGTTCTTCCAGGTCGTGAACCACGGCGTGGACCCGGCGCTGCTCGCCAAGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence analysis see http://www.genome.clemson.edu/projects/barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 571;
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Pred. No. 1.7e-31;
0; Mismatches 127
                     'organism="Hordeum vulgare"
                                                                                               /clone="HVSMEh0095D08f"
                                          /cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%;
illarity 69.3%;
Conservative
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Best Local S
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BE422495/c
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                                                                                                                                                                                                                                                                                                              EST 01-MAR-2001
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons; core eudicots,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1420 TCGACACGCTGGGCACCGGTCCGCACTGCGACCCCCACCTCGCTCACCATCCTCCACCAGG 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1540 CCGGGGCGCTCGTCGTCACGTCGGCGACACCTTCATGGCGCTCTCCAACGCCAGGTACC 1599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 TCAATGCATTTGTGGTTAACATAGGCGACACATNTATGGCGCTATCAAATGGAAGATACA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 AAAGTIGCCIGCACAGAGCAGIAGIAAACAACAAGACICCIAGAAAAICACIIGCIIICI 308
                                   516
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                                                                                                                                                                                                                                                                                                           BG350197 655 bp mRNA linear EST 01-1
084C04 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
Emmersen, J. and Welinder, K.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                          1243 TGGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCTGTCGCTGG 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 655)
Nielsen,K.L, Crookshanks,M., Emmersen,J. and Welinc
EST-sequencing of mature potato tuber (Var. Kuras)
Unpublished (2000)
Contact: Karen G. Welinder
Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 others
                                                                                                                             Pred. No. 4.5e-30;
0; Mismatches 174; Indels
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Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Solanum tuberosum'/cultivar="Field grown Kuras'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Tuber"
/note="Vector: Lambd
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Fax: +45 98141808
Emall: Kgw@blo.auc.dk
Sequenced from the 5' end.
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                              GI:13178939
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Matches 300; Conservative
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ORIGIN
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TITLE
JOURNAL
                                                                                                                                                                                                                                              RESULT 12
BG350197
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

7 Triticeae; Triticum.

Altenbach, S., Anderson, O.D., Chao, S., Gallli, G., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and
                                                                                                                                                                                                                                                                                          BE422495 517 bp mRNA linear EST 24-JUL-2000 WHE0056_E02_104ZS Wheat endosperm cDNA library Triticum aestivum cDNA clone WHE0056_E02_104, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: Lambda ZAP II, excised phagemid; Site_1: BcoRI; Seeds collected, endosperm isolated, and RNA prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The structure and function of the expressed portion of the wheat
1720 ACCCGAGGGTGTACCCGGACTTCACGTGGCGGGCGCTGCTGGACTTCACGCAGCGCCCACT 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1460 GCTCACCATCCTCCACCAGGACCACGTCGGCGCCTGGAGGTGTGGGCGGAGGGGGCGGTG 1519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
                            1780 ACAGGGCCGACATGCGCACGCTTCAGGCCTTCCCGACTGGCTTAATCATCATC 1833
                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 191.2; DB 10; Length 517;
Pred. No. 6.6e-29;
0; Mismatches 103; Indels 3;

    .517
    /organism="Triticum aestivum"

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BE422495.1 GI:9420410
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Similarity 71.5%;
56; Conservative (
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GA_EG052C12f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ed0052C12f, mRNA sequence.
BQ402912.1 GI:21090599
                                                                              943 CGIGCGAGAGGCACGGCTICTICCTGGTGGTTAACCACGGCAICGAGGCGGCGCTGCTGG 1002
                                                                                                                                                                                                                                                   CGCAGCGGCGCGCGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGGGCGCTTCGCGT 1122
                                                                                                                                                                                                                                                                                                                                    1123 CCAAGCTGCCGTGGAAGGAGACGCTGTCGTTCCGGTACTCATCGGCTGGAGATGAAGAGG 1182
                                                                                                                                                               1003 AGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGGAGAAGCAGCGGG 1062
                        279 TCGCCGGGTTCCTGGCGGGCGACGGCGCTGCCACTGGCGGCCTCCGTGACCTGGCCGCCG 338
                                                                                                                                                                                     459 CGCAGCGCCGCCTCGGCGAGAACCACGGGTACGCCGCCAGCTTCGTGGGGCGGGGTCGGCA 518
                                                                                                                                                                                                                                                                                                                                                         TGG------GGGCGGGGGGGGGGAGGTCGTCGGTGG--TCCGGCAGGTGGGGGAGG 942
                                                                                                  100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
Total High Quality bases = 572
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 7
High quality sequence stop: 680.
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AUTHORS
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BQ402912
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                              BE414214 686 bp mRNA linear EST 24-JUL-2000 SCU007.E01.R990714 ITEC SCU Wheat Endosperm Library Triticum aestivum cDNA clone SCU007.E01, mRNA sequence.
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Anderson.O.A. Appels R., Bailey, P., Blake, T., Close, T., Cloutier
Anderson.O.A. Appels R., Bailey, P., Blake, T., Close, T., Cloutier
S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
Herrmann, R.G., Holton, T., Jaquemin, J. M., Jia, J., Joudrier, P.,
Langridge, P., Lazo, G. R., Lin, J., McGuire, P., Ogihara, Y.,
Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Holton T'
Centre for Plant Conservation Genetics, Southern Cross University
PO Box 157, Lismore NSW 2480 AUSTRALIA
Tel: 61 2 6620 3409
Fax: 61 2 6622 2080
          1757 GCTGGACTTCACGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGA 1816
                                217 CCTCGAGTTCACGCAGAAGCACTACCGCTCTGACTGGAGGACCCTGGATGCATTCGCCTC 158
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                                                                                                                    277 CGAGCTGCTCGCCGTCGACGCCCCCGCGCGTGTACCCCGGACTTCACTTGGCGTGAATT
                                                                                                Score 187; DB 10; Length 686;
Pred. No. 4.6e-28;
0; Mismatches 126; Indels 12;
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/clone_lib="TPEC_SCU Wheat Endosperm Library"
/tissue_type="endosperm"
/note="Vector: Bluescript II SK(-)"
232 c 232 g 105 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    International Triticeae BST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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/cultivar="Wyuna"
/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE414214.1 GI:9412060
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Best Local Similarity 68.1%;
Matches 294; Conservative
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Duraryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta, Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosidas II; Malvales; Malvaceae; Gossypium.

1 (Dases 1 to 700)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leelle,A. and Wilkins,T.A.

In the corton fiber
Unpublished (2000)
Contact: Wing R.A.
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="8400"
/db_xref="taxon:39729"
/clone="64_Re0052c129"
/clone=1ch="cossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 185.6; DB 14; Length 700;
Pred. No. 8.8e-28;
0; Mismatches 230; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI" 148 c 171 g 186 t 1 others
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Best Local Similarity 59.9
Matches 371; Conservative
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1168 CTGGAGATGAAGAGGCGAGGAGGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGGCGG 1227
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                                                                        988 AGGCGCCCCCCCGCAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGG 1047
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928 GECAGGIGGGGAGGCGIGCGAGAGGCACGGCTICTICCIGGIGGITAACCACGGCAICG 987
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Search completed: March 26, 2003, 07:52:50 Job time: 2570.09 secs

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) ORGANISM: Arabidopsis thaliana; IMMEDIATE SOURCE:
CLONE: pat2301
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                   GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-209-747-1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 1
Sequence 1
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Patent No. 2539539
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
US-08-458-298-1
US-09-454-034-9
US-08-25-3674-12
US-09-734-719-12
US-09-734-719-12
US-08-76-9078-1
US-08-76-9078-1
US-08-117-844B-1
US-08-232-466-1
US-08-232-9868-1
US-08-823-9868-1
US-08-823-9868-1
US-08-823-9868-1
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US-08-823-9868-1
US-08-823-9868-1
US-08-823-9868-1
US-08-823-9868-1
US-08-823-9868-3
US-08-823-9868-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-10403-3
US-09-615-192A-149
US-09-010-928B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/553,367A
FILING DATE: No. 5939539ember 27, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONEY AGENT INFORMATION:
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 49/FD4.5MZ
TELEPCOMUNITATION INFORMATION:
TELEPERONE: 202-721-8200
TELEFAX: 202-721-8250
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                                                                                                                                                  174
888
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STATE: D.C.
COUNTRY: U.S.A.
TP: 20006
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999 CIGGAGGAGGCGCACCGGIGCAIGGACGCCIICIICACGCIGCCGCIGGGGGAGAAGCAG 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1259;
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Pred. No. 2.2e-54;
0; Mismatches 336;
                   Lind & Ponack, L.L.P. N.W., Suite 800
                                                                                                                                                    윝
                                                                                                                                                                                                                                                                                                                                                                    NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 49/DIV-FD4.5MZ
TELECOMBUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                     1995
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPOTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOOGPETCET 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,306
                                                                                                                                                                                                                                                                                                                                     27,
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6198021ember ;
ATTORNEY/AGENT INFORMATION:
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nilarity 60.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                       2033 K Street,
                       Wenderoth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                 ADDRESSEE: Wender
STREET: 2033 K St
CITY: Washington
                                                                            D.C.
: U.S.A.
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Best Local Sim:
Matches 532;
                                                                                             COUNTRY:
                                                                          STATE:
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                                                                                                                                                CTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGAGAAGCAG 1058
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                                                                      939 GAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGGCGCTG 998
                                                                                             324 ATATCAGACGCTCATGAATACACGAGCCGCTTCTTTGATATGCCTCTCTCCGAAAAAGAG 383
                                       Gaps
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                                     18;
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APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NOMBER OF SEQUENCES: 19
 Length 1259;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1779 TACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTA 1824
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Score 292.4; DB 2;
Pred. No. 2.2e-54;
0; Mismatches 336;
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Patent No. 6198021
11.7%;
60.0%;
                                     Conservative
                 Similarity
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Local 5-
532;
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US-09-295-306-3
Query Match
                   Best Loca
Matches
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LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                               11.7%;
                                                                                                                                                                                                                                           Best Local Similarity 60.0 Matches 532; Conservative
                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                 HYPOTHETICAL: NO
                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                  US-09-734-719-3
                                                                                                                                                                                                                               Query Match
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       1359 TICTICCAGGGGAACGACTCCATCATGCGCCTCAACTACTACCGGGGGTGCCAGAGGCCA
                          786 GACCAIGTTAATGGCCTTCAAGTCTTTGTGGAAAATCAATGGGGCTCCATTGGTCCAAC
                                                                                                                                                                               1539 CCCGGGGCGCTCGTCGTCGACGTCGGCGACACCTTCATGGCGCTCTCCAACGCCAGGTAC
                                                                                                                                                                                                966 TICTTGTGTCGAAAAAGACAGAGTAGTGACGCCACCGAGAGAGCTTTGGACAGCATC
                                                                                                                                                                                                                                       APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
                                                                                                                                                                                                                                                                                                                                                                                                                          1779 TACAGGGCGACATGCGCATGCTTCAGGCCTTCTCCGACTGGCTTA 1824
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ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREFT: 2033 K Street, N.W., Suite 800 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2000-1678/LC/01784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/295,306
FILING DATE: APPLI 12, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6455675ember 27,
APPLICATION NUMBER: PCT/EF94/01664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/734,719
FILING DATE: 13-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09734719
Patent No. 6455675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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APPLICANT: Theo
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US-09-734-719-3
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                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                  Length 1259;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                           Score 292.4; DB 4;
Pred. No. 2.2e-54;
0; Mismatches 336;
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ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
                                                                                                       CLONE: PAt2301
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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ACGICGCCGACACCITCATGCCGCTCICCAACGCCAGGIACCGCAGCTGCCTGCACCGGG 1617
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                          958 GCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGGCGCTGCTGGAGGAGGCGCACCGGT 1017
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US-09-295-306-5
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778 IGITCGACGCGCGGTGCTGAGCGGGCAGACGGAGATCCCGTCGCAGTTCATATGGCCGG 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                         Sequence 5, Application US/08553367A
Patent No. 2839539
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 271; DB 2; Length 1490;
Pred. No. 1e-49;
0; Mismatches 435; Indels 2
                                                                              1086 TATAGAGCAGACATGAACACTCTCCAAGCCTTTTCAGATTGGCTCA 1131
                                                        1779 TACAGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTA
                                                                                                                                                                                                                                                                                                                             Wenderoth, Lind & Ponack, L.L.P. 33 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM COmpatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CUBRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/553,367A
FILING DATE: No. 5939539ember 27, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE;
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                             STREET: 2033 K Street, N.W., CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 56.5
Matches 593; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800
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                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                       RESULT 4
US-08-553-367A-5
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                                                                                                                                                                                                                                                                                                                                                                 CITY: 1
STATE:
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586 AAGAITACTITICCGATACATTAGGACAAGAGTTCG---AGCAGITTTGGGAAGGTGTATC 642
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ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/295,306
FILING DATE: April 21, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6455675ember 27,
APPLICATION NUMBER: PCT/EP94/01664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/734,719
FILING DATE: 13-Dec-2000
CLASSIFICATION: <UNKnown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1078 GGGAGAGCIGCGGCIACGCCAGCACTICACGGGGCGCTICGCGICCAAGCIGCCGIGGA 1137
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                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                  NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKEY NUMBER: 49/DIV-FD4.5MZ
FELECOMMUNICATION INFORMATION:
TELEFRONE: 202-721-8200
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6198021ember 27, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LANGTH: 1490 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
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56.5%;
                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
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                                                                             COMPUTER READABLE FORM:
                    D.C.
: U.S.A.
Washington
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Best Local Similarity
Matches 593; Conserv
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                                                                                                                                                                                                                      FILING DATE:
                                                        20006
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US-09-295-306-5
                                         COUNTRY:
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1054 ACAAAGTGGTGAAACCACCAAGTGATATTTTGGAGAAGATGAAAACAAGAAAATACCCTG 1113
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                                                                                                                                       GCCTGGGCATCGTCGAGACCGGCGCCACTACTTCCGGCGATTCTTCCAGCGCAACGACT 1377
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Patent No. 6455675
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
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1438 GTCCGCACTGCGACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGGCCTGG 1497
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
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NAME: Lee Chenq
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TELEFAX: 202-721-8250
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TYPE: nucleic acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STREET: 20
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US-08-553-367A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 271; DB 4; Length 149
Pred. No. 1e-49;
0; Mismatches 435; Indels
                                                 REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2000-1678/LC/01784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                    CLONE: PAT2353
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FILING DATE: May 24, 1994
                 ATTORNEY/AGENT INFORMATION: NAME: Lee Cheng
                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.8%;
Best Local Similarity 56.5%;
Matches 593; Conservative
                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-734-719-5
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CGGTTGTGAATAGAGAGAGCGCGAGAAATCGATGGCGTTTTTTCTTGTGTCCGAAGAAAG 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTICACGIGGCGGCGCTGCTGGACTTCACGCAGCGCCCACTACAGGGCCGACATGCGCA 1797
                                                                                   AGGIGIGGGCGGAGGGCGGTGGCGCCCATCCGCCCTCGCCCCGGGGCGCTCGTCGTCA 1557
                                                                                                                                                                                                      CGGTCGTCAACAGCACGGCGCCTCGCCGCTCGCTGGCCTTCTTCCTCTGCCCGGAGATGG 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACGGTGGTGCCCCCCCCCGCAGGAGCTGGTCGACCACCACCCGAGGGTGTACCCGG 1737
                                                                                                                            934 ATAITGGTGACACTTTCATGGCTCTATCGAACGGGATATTCAAGAGCTGTTTGCATAGAG 993
Sequence 1, Application US/08553367A
Patent No. 5939539
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCTTCAGGCCTTCTCCGACTGGCTTAAT 1826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1648 CGCTGGCCTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGCGCCGCCGCCGGAGGAGCTGG 1707
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                                                                                                                                                                                                                                                                                                                                                                  1048 GGGAGAAGCAGCGGCGCAGCGGCGCGCGGGGAGAGCTGCGGCTACGCCAGCAGCTTCA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGGCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGCCTGTCGTTCCGGTACTCATCGG 1167
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                                                                                                                        Length 1395;
                                                                                                                                                              Indels
                                                                                                                      Score 226.4; DB 2;
Pred. No. 4.5e-40;
0; Mismatches 381;
                   ORGANISM: Cucurbita maxima IMMEDIATE SOURCE: CLONE: Clone pB11
                                                                                                                      9.1%;
ilarity 55.2%;
Conservative
                                                                                                                   Query Match
Best Local Similarity
Matches 496; Conserv
ORIGINAL SOURCE:
ORGANISM: CUC
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US-08-553-367A-1
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RESULT 8 US-09-295-306-1

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                                                                    Theodor LANGE et al. VENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
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55.2%; Pred. No. 4.5e-40;
tive 0; Mismatches 381;
                                                                                                                                                   & Ponack, L.L.P., Suite 800
                                                                                                                                                                                                                                                                                                     đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOKNEL Lee Cheng
REGISTRATION NUMBER: 40,949
REGISTRATION NUMBER: 49/DIV-FD4.5MZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NONBER:
FILING DATE: NO. 6198021ember 27, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       inch, 1.44
                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WOADDEFIECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,306
Sequence 1, Application US/09295306
Patent No. 6198021
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDA,
NUMBER OF SEQUENCES: 19
                                                                                                                                                                        2033 K Street, N.W.,
                                                                                                                                                      Lind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 202-721-8200 TELEFAX: 202-721-8250
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nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                         IBM Compatible
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                 CORRESPONDENCE ADDRESS
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CLONE: Clone pB11
                                                                                                                                                                                                              STATE: D.C. COUNTRY: U.S.A. ZIP: 20006
                                                                                                                                                                                               Washington
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-295-306-1
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1588 ACGCCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCCGCT 1647
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                                                                    1288 CGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCATCGTCGGAGACCGGCGCCACT 1347
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1768 CGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAA 1825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (AS Amended)
NUMBER OF SEQUENCES: 19
                                                                                                                    595 GTACGAAGATTGTGGAGCTTTTGGGGCCTTTGGCCATTTCAAGAG-----AAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPETECT 5.1
CURRENT APPLICATION DATA:
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FILING DATE: APTIL 21, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: NO. 6455675cmber 27, 34PLICATION NUMBER: PCT/EP94/01664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/734,719
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09734719
Patent No. 6455675
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
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ZIP: 20006
COMPUTER READABLE FORM:
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                    ATCATGGG
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REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2000-1678/LC/01784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 226.4; DB 4
Pred. No. 4.5e-40;
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Cucurbita maxima
                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERICATICS:
LENGTH: 1395 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                         TELEFAX: 202-721-8250
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                                                                                                                TELEX: <Unknown>
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                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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1648 CGCTGGCCTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGCTGCCCCGCCGGAGGAGCTGG 1707
                                                               TCGACGACCACCACCGGGGGGGGTGTACCCGGACTTCACGTGGCGGGGGGCGTGCTGGACTTCA 1767
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GENERAL INFORMATION:
APPLICANT: HOTLICK, ROBERT
TILLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/09055
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       752 Gergergeageageagergergrerreaceageceergergeagegeagaegea
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49.2%; Pred. No. 1.9e-11;
tive 0; Mismatches 256;
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CTHER INFORMATION: coding strand of EBNA-1 DNA US-09-249-585A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Epstein Barr Virus
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                                                                                                                                                                                                       RESULT 10
US-09-249-585A-2
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1052 GAAGCAGCGGCGCAGCGGCGCGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGG 1111
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                                                   GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94.4; DB 3; Length 2
Pred. No. 2e-11;
0; Mismatches 256; Indels
                                                                                                                                                                                                        ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDION TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/050,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A-65638/DJB/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09050863; Patent No. 6114111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SILVa, RODIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-1
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1998
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LENGTH: 2580 base pairs
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Matches 248; Conservative
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STRANDEDNESS: unknown
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                   94111-4187
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                                                                                                                                                                                                                                                                                   USA
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US-09-050-863-2
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US-09-050-863-2
                                                                                                                                                                                                                                                                                   COUNTRY:
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/130,114 CURRENT FILING DATE: 1998-08-06
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Best Local Similarity 49.2
Matches 248; Conservative
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ORGANISM: VEBNA
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                                                                                                          1172 AGATGAAGAGGCCGAGGAGGCCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCGGAGCA 1231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Mammalian Protein Interaction Cloning System
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ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
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COMPUTER READABLE FORM:
COMPUTER: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-01-1999
CLASSIFTCATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS TELECOMMUNICATION INFORMATION:
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Pred. No. 2e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                 1173 GGAGGGCAGGAGGGCAGGAGCA 1196
                                                                                                                                                                                                                                                                             1232 CGGCGGCGCTGGGCGAGGTGTA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09359081
Patent No. 6316223
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2580 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: <Unknown> artorner/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       949-8711
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STRANDEDNESS: unknown
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Hiang, Betty
Payan, Don
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Best Local Similarity
Matches 248; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-359-081-2
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                                                                                                                        GGTGGGGGAGGCGTGCACACGCCTTCTTCCTGGTGGTTAACCACGGCATCGAGGC
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Patent No. 5976807

GENERAL INPORMATION:
APPLICANT: HOLICK, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Enkaryotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/ID903U51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 2.6e-11;
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1052 GAAGCAGCGGCGCAGCGGCGCGCGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGG 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                               992 GGCGCTGCTGCAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGA 1051
                                                                                                                                                                                                                                                                                                                                                                                      932 GGTGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGC 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zuckermann et al. TITLE OF INVENTION: Compositions and Methods for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Jul-2000
CLASSIFICATION: <UNKNOWN>
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MOLECTIE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-620-925-1
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ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: CURKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: FUJILA, SHATON M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1219 GGAGGGCAGGAGGGCAGGAGCA 1242
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TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1232 CGGCCGCCGCTGGGCGAGGTGTA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-620-925-1
; Sequence 1, Application US/09620925
; Patent No. 668986
; GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions and Methods for
Polynucleotide Delivery
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49.2%; Pred. No. 3.2e-11;
tive 0; Mismatches 256;
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                                                                                                                                                                                                                                                                                                                       1632 GCAGGGCAGGAGGGCAGGCA 1609
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ADDRESSEE: Chiron Corporation
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ATTORNEY/AGENT INFORMATION:
NAME: FUJITA, Sharon M.
REGISTRATION NUMBER: 38,459
REFERNCE/POCKET NUMBER: 1218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-910-647-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Composit
TITLE OF INVENTION: Polynucl
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TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
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Matches 248; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                           Gaps
                                                    752 GETGGTGCAGCAGCAGCAGGTGGTGTTCGACGCGGCGGTGCTGAGCGGGCAGACGGA 811
                                                                                                        812 GATCCCGTCGCAGTTCATATGGCCGGCGGAGGAGAGCCCCGGGTCGGTGGCGGTGGAGGA 871
                           0;
3.8%; Score 94.4; DB 4; Length 9600;
49.2%; Pred. No. 3.2e-11;
tive 0; Mismatches 256; Indels 0
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Matches 248; Conservative
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                                                                                             March 26, 2003, 05:23:30 ; Search time 137.899 Seconds
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Mo. Score Match Length DB ID Description Description Match Length DB ID Sequence 77, Appl 2 153.2 6.1 1077 10 US-09-371-307-77 Sequence 77, Appl 3 129 5.2 811 10 US-09-371-307-71 Sequence 77, Appl 8 4.8 3.4 .12733 9 US-10-032-393-8 Sequence 77, Appl 5 84.8 3.4 .12733 9 US-10-032-393-8 Sequence 87, Appl 6 81.2 3.2 266 10 US-09-938-842A-812 Sequence 1829, Appl 7 10 US-09-938-842A-151 Sequence 1829, Appl 10 US-09-938-842A-151 Sequence 1829, Appl 10 US-09-938-842A-151 Sequence 1821, Appl 10 US-09-938-842A-151 Sequence 19241, Appl 10 US-09-938-842A-151 Sequence 26672, Appl 11 77 2 2.9 1076 10 US-09-98-644-761-2009 Sequence 2672, Appl 12 71.6 2.9 1075 10 US-09-864-761-2009 Sequence 2673, Appl 12 71.4 2.9 1852 10 US-09-864-761-2013 Sequence 2513, Appl 12 71.4 2.9 1852 10 US-09-864-761-2014 Sequence 2731, Appl 12 71.4 2.9 1852 10 US-09-864-761-2014 Sequence 2731, Appl 12 71.4 2.9 1852 10 US-09-864-761-2014 Sequence 2731, Appl 12 2.7 1973 10 US-09-988-842A-161 Sequence 1691, Appl 12 2.7 1973 10 US-09-864-761-2021 Sequence 1691, Appl 13 0 US-09-881-842A-1691 Sequence 1691, Appl 14 71.4 2.9 1852 10 US-09-881-842A-1691 Sequence 1691, Appl 14 0 US-09-881-842A-1691 Sequence 1691, Appl 15 0 US-09-981-842A-1691 Sequence 1691, Appl 15 0 US-09-981-842A-1691 Sequence 1691, Appl 15 0 US-09-881-842A-1691 Sequence 1691, Appl 15 0 US-09-881-842A-1691 Sequence 1691, Appl 15 0 US-09-981-842A-1691 Sequence 1691, Appl 15 0 US-09-981-842A-1691 Sequence 1691, Appl 15 0 US-09-881-842A-1691 Sequence 1691, Appl 15 0 US-09-981-842A-1691 Sequence 1691,

48 Sequence 48, Appl 48 Sequence 48, Appl 48 Sequence 48, Appl 49 Sequence 39, Appl 2267 Sequence 2267, Ap 2267 Sequence 2267, Ap 2267 Sequence 129, Appl 2268 Sequence 1529, Ap 291 Sequence 19531, Appl 2921 Sequence 19531, Appl 2032 Sequence 16, Appl 2040 Sequence 16, Appl 2058 Sequence 16, Appl 2058 Sequence 16, Appl 2058 Sequence 16, Appl 2058 Sequence 168, Appl 2058 Sequence 1058, Ap 2058 Sequence 238, Ap 2058 Sequence 268, Appl 2058 Sequence 2784, Appl 2058 Sequence 2787, Appl 2058 Sequence 1, Appli 205	gibberellin levels	tch al Similarity 55.2%; Pred. No. 1.4e-50; Length 1161; 496; Conservative 0; Mismatches 381; Indels 21; Gaps 2; 6GCAGGTGGGGAGGCAGGTTCTTCTGGTGGTTAACCAGGGATCG 987 11111111111111111111111111111111111
US-09-976-740-48 US-10-023-529-48 US-10-023-523-48 US-09-864-761-3936 US-09-38-842A-2267 US-09-938-842A-1529 US-09-98-842A-1529 US-09-864-761-19531 US-09-864-761-19531 US-09-864-761-768 US-09-85-288A-1 US-09-85-288A-1 US-09-85-288A-1 US-09-85-288A-1 US-09-85-288A-1 US-09-85-288A-1 US-09-85-288A-1 US-09-82-273-1658 US-09-93-27A-1658 US-09-93-842A-2398 US-09-93-876-2158 US-09-93-876-2158 US-09-93-876-2158 US-09-93-876-111844 US-09-93-876-761-11844 US-09-93-876-761-11844 US-09-93-876-761-11844	ALIGNMENTS US/09371307A A1 I M. Y R. tth J. Seah M. D. nne W. nnla rry J. ndds for controlling 6 BER: US/09/371,307A 99-08-10 2.0	Score 226.4; D Pred. No. 1.4e- 0; Mismatches GAGGCACGCCTTCTCC
2561 9 2561 12 2561 12 2561 12 1003 9 1004 10 1008 9 1007 9 4257 9 4257 9 4257 9 15720 9 115720 9 115720 9 115720 10 165 9 247 10 2482 10 165 9	SEGUT 1 S-09-371-307-77 Sequence 77, Application US/09: Patent No. US2002005309541 GENERAL INFORMATION: APPLICANT: Brown, Sherri M. APPLICANT: Piller, Kenneth J. APPLICANT: Piller, Kenneth J. APPLICANT: Piller, Kenneth J. APPLICANT: Piller, Kenneth J. APPLICANT: APPLICANT: Roab Ganesh M. APPLICANT: Roab Ganesh M. APPLICANT: Logusch, Eugene W. APPLICANT: Roab Ganesh M. APPLICANT: Logusch, Sherry J. TILLE OF INVENTION NUMBER: UGURENT FILING DATE: 199-08-NUMBER OF SEQ ID NOS: 89 SOFWARE: Patentin Ver. 2.0 LENGTH: 1161 TYPE: DNA GRAANISM: CUCURDITA MAXIMA S-09-371-307-77	9.1%; rvative AGCCGCGA AGCCTGCGA IIII IIIIII IGGGCCGTGT IGGGCCGTGT IIIIIII
	307-77 10. US2002205305A1 INFORMATION: NRT: Brown, Sherri M. NRT: Heck, Gregory R. NRT: Piller, Kenneth J. NRT: Elich, Tedd D. NRT: Elich, Tedd D. NRT: Elousch, Eugene W. NRT: Logusch, Sherry J. NRT: Logusch, Sherry J. FILING DATE: 1999-08 OF SEQ ID NOS: 89	h. Similarity 96; Conser CagGrGGGGGA CAGGGGGGATGA CAGGGGGGGGGGGGGGGGGG
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                                                                                                                                    CTGGAGATGAAGAGGGCGAGGAGGGCGTGGGTGCTACCTGGTGCGGGAAGCTCGGGGCGG
                                                                                                                                                                                                   473 CICAAAACICCICCGGGGCICARGACIAIGIICTIGACACITIAGGCCCAICATTCICCC
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1108 CGGGCCCTTCGCGTCCAAGCTGCCGTGGAAGGACGCTGTCGTTCCGGTACTCATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brown, Sherri M.
APPLICANT: Brown, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Ream, Joel B.
APPLICANT: Ream, Joel E.
APPLICANT: ALTOGRAPH AND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/371,307A CURRENT FILING DATE: 1999-08-10 NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09371307A Patent No. US20020053095A1
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Pred. No. 7e-31;
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CTHER INFORMATION: n US-09-371-307-8
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Sequence 71, Application US/09371307A

Sequence 71, Application US/09371307A

Sequence 71, Application US/09371307A

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APPLICANT: Elich, Tedd D.

APPLICANT: Logusch, Eugene W.

APPLICANT: Ream, Joel E.

APPLICANT: APPLICATION NORBER: US/09/371,307A

SOUTRENT FILING DATE: 1999-08-10

SOUTHARE: Patentin Ver. 2.0

SECIID NOS: 89

SOUTHARE: Patentin Ver. 2.0
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Pred. No. 1.9e-24;
0; Mismatches 205;
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APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT PILLING DATE: 2000-112-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 9.2e-12;
0; Mismatches 342; Indels
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; OTHER INFORMATION: Vector pEPEF14
US-10-032-393-47
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ORGANISM: Artificial Sequence
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Best Local Similarity 45.95
Matches 290; Conservative
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GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Manigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLINUCLEOTIDES AND POLIPEPTIDES DERIVED FROM CORN SEEDLING
FILE REPRENCE: PL-0012-1 CON
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-05-05
PRIOR FILING DATE: 1998-05-05
SOFWRAKE: PERL PROGram
SEQ ID NO 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joe1
APPLICANT: Kang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAININ
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1382 CATGCGCCTCAACTACTACCCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGTCC 1441
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| NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20020013958A1 700159601H2
| US-09-923-876-1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81.2; DB 10; Length
Pred. No. 6.6e-12;
0; Mismatches 58; Indels
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-05-22
Sequence 812, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                           Sequence 1829, Application US/09923876
Patent No. US20020013958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2%;
Best Local Similarity 67.9%;
Matches 129; Conservative
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US-09-938-842A-812
                                                                                                                      JS-09-923-876-1829
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                                                                                                       APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
FILE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA,010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT APPLICATION NUMBER: 60/259,434
PRIOR PILING DATE: 2000-12-27
PRIOR PLING DATE: 2001-12-27
PRIOR PLING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR PLING DATE: 2001-09-06
PRIOR PLING DATE: 2001-09-06
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                           Sequence 8, Application US/10032393
Publication No. US20030027286A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Vector peper1
US-10-032-393-8
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                                                                                            GENERAL INFORMATION:
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RESULT 9
US-09-294-093B-5184
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFREENCE: SCRIPTIANO-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/238,842A
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-10-16
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                                                                                                                                                                                                                                                                                    111 CTATGGCGTGAATAGTGGTTTTAAGTGCTGGTCTTGGTATTGGTGGTGGTCCTTGG 170
                                                                                                                                                                                                                                                                                                                                                                              171 AGAGGATCTGGTTACGGAGGTGGAAGCGGTGAAGGCGGTGGAGCTGGTGGGCATGGCGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                         700 CCATCGGTTAATTAATTGATTGATAGCTAGATTATCAACAATTAATGAGCATGGTGGTGC 759
                                                                                                                                                                                                                                                                                                                                    760 AGCAGGAGCAGGAGGIGGIGIICGACGCGGCGGIGCIGAGCGGGCAGACGGAGAICCCGI 819
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                                                                                                                                                DB 9; Length 768;
                                                                                                                                           Score 80; DB 9; Length 768
Pred. No. 2.8e-11;
0; Mismatches 330; Indels
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                            TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                              3.2%;
                                                                                                                                           Query Match 3.2%
Best Local Similarity 46.7%
Matches 294; Conservative
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                                                                          ; ORGANISM: Arap;
US-09-938-842A-812
SEQ ID NO 812
LENGTH: 768
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APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLITYCLEOTIDES AND POLITEPTIDES DERIVED FROM CORN TASSEL
TITLE OF INVENTION: POLITYCLEOTIDES AND POLITEPTIDES DERIVED FROM CORN TASSEL
CURRENT PLICATION UNMER: US/09/294,093B
CURRENT APPLICATION NUMBER: 09/062,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL PROGram
LENGTH: 276
LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1450 ACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGGCCCTGGAGGTGTGGGGCGG 1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1630 GCACGGCGCTCGCCGCTCGCTGGCTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGC 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              980 CTACAAAACCTAGGATATCGGTGGCGTCGCTACACAGCTTCCCTTTGACTTCTGTCGTAA 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     860 GIGACGAGTGGGTCACCGTTGATCCCATCCCTGGCTCTTTGTTGTCAACGTAGGCGATC 919
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920 ATCTCGAGATATTTAGCAATGGGAGGTATAAAAGCGTGCTACATAGGGTATTGGTGAACT
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                                                                                                                                                                                                                                            Length 1179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1040 AGCCATCGCCGAAACTCGTCGATAAACATAATCCATCACAGTATATGGAC 1089
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700355956H1
NAME/KEY: unsure
                                                                                                                                                                                                                                      Score 74.8; DB 9; Length 1:
Pred. No. 9.4e-10;
0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 73.2; DB 10;
56.2%; Pred. No. 9.7e-10;
iive 0; Mismatches 105;
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; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-5184
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1511
LENGTH: 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5184, Application US/09294093B Patent No. US20010051335AI GENERAL INFORMATION:
APPLICANT:
Lalgudi, Raghunath, V.
                                                                                                                                                          ; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1511
                                                                                                                                                                                                                                         3.0%;
                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 50.99
Matches 178; Conservative
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nes 135; Conserv
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ORGANISM: Zea mays
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 CAATTAATGAGCATGGTGGTGCAGCAGGAGCAGGTGGTGTTCGACGCGGGGGGTGCTG 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9%; Score 73; DB 10; Length 446; 50.7%; Pred. No. 1.5e-09; ive 0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N: EXPRESED IN HEART, SIGNAL = 10
N: EXPRESED IN FETAL LIVER, SIGNAL = 14
EXPRESED IN LUNG, SIGNAL = 13
N: EXPRESED IN HELLOO, SIGNAL = 12
N: EXPRESED IN HELA, SIGNAL = 13
N: EXPRESED IN PLACENTA, SIGNAL = 13
N: EXPRESED IN PLACENTA, SIGNAL = 13
N: EXPRESED IN BT474, SIGNAL = 13
N: EXPRESED IN BTA14, SIGNAL = 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2000-09-21
PRIOR FILLING DATE: 2000-09-21
PRIOR FILLING DATE: 2000-09-30
PRIOR FILLING DATE: 2000-09-30
PRIOR FILLING DATE: 2000-09-30
PRIOR FILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                                                                     DR FILING DATE: 2000-05-26

DR APPLICATION NUMBER: US 09/632,366

DR APPLICATION NUMBER: GB 24263.6

DR APPLICATION NUMBER: GB 24263.6

DR FILING DATE: 2000-10-04

DR APPLICATION NUMBER: US 60/236,359

DR FILING DATE: 2000-09-27
                                                                                                                                                                                                                    FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00665
FLIJING DEFE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCI/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCI/US01/00667
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
FEAGURE:
OTHER INPORMATION: MAP TO AC007249.2
                                                     APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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US-09-864-761-20699
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Matches 175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1442 GCACTGCGACCCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGCCTGGAGGT 1501
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                                                                                                                                      1510 AGGGGCGGTGGCGCCCATCCGCCCTCGCCCCGGGGCGCTCGTCGTCACGTCGCCGACA 1569
                                                                                                                                                                                                                                                     1502 GTGGGGGAGGGGCGGTGGCGCGCCATCCGCCCTCGCCCCGGGGCGCTCGTCGTCAACGT 1561
                          1450 ACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGCCTGGAGGTGTGGGCCG 1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660 ACATAAAAGACCCAACCGTTATCACTTCTTCTACAAGACCAAGTCTCTGGTTTGCAAGT 719
                                                                                                                                                                             156 ATGGTCAATGGTACGAGGCCAAGTACGTGCCCGACGACTCATCGTCGTATCGGCGATC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600 CATGGCGTTTAACTACTATCCGCCGTGTCCAGAACCCGAGCTAACTTACGGACTTCCCGG 659
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                                                                                                                                                                                                                                                                                                             216 AGAICGAGATTITCAGCAACGGGGCATACAAGGCGGTGCTGCACCGTACGACGGTGAACA
                                                                             96 ACATGAGCACGCTCACCTTCGTGCCCAACGAGGTGCAGGGGCTCCAGGTCTTCAAAG
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Pred. No. 2.3e-09;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REPERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR PFLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2010-16
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US-09-864-761-20699
; Sequence 20699, Application US/09864761
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2672, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Arabidopsis thaliana
US-09-938-842A-2672
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illarity 50.9%;
Conservative
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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Best Local Similarity
Matches 174; Conserv
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US-09-938-842A-2672
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LENGTH: 1050
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991 CGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGG 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1171 GAGATGAAGAGGCGAGGAGGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCGGAGC 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1231 ACGGGCGGCGCCTGGGCCAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCTGTCGC 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 TGGTGATGGTGATGGTGGTAGTAGTGGTAGTGGTGATGCTGGTGGTGGTGGTGGTGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 811 AGAICCCGICGCAGTICAIAIGGCCGGCGGAGGAGAGCCCCGGGTCGGTGGCGGTGGAGG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               931 AGGIGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGG 990
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OTHER INFORMATION: EXPRESED IN BUNG, SIGNAL = 19
OTHER INFORMATION: EXPRESED IN BUNG, SIGNAL = 34
OTHER INFORMATION: EXPRESED IN BUT44, SIGNAL = 3.4
OTHER INFORMATION: EXPRESED IN PETAL LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESED IN ADULT LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 2.0
OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESED IN HEART, SIGNAL = 2.5
OTHER INFORMATION: EXPRESED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: THE ALIGNAL SIGNAL = 2.1
OTHER INFORMATION: WHIT: ALIGNAL SIGNAL = 2.1
OTHER INFORMATION: WHIT: ALIGNAL SIGNAL = 2.1
OTHER INFORMATION: WHIT: ALIGNAL SIGNAL = 2.1
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NUMBER OF SEQ ID NOS: 49117
SOFTMARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 19241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.9%; Score 71.6; DB 10; 45.2%; Pred. No. 6.4e-09;
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US-09-864-761-2513
US-09-864-761-2513, Application US/09864761;
Patent No. US20020049763A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                   TYPE: DNA
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hangel, David R.
APPLICANT: Hangel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     978 CACGGCAICGAGGCGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACG 1037
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798 AGCGGCAGACGGAGATCCCCGTCGCAGTTCATATGGCCGGGGGAGGAGGCCCCGGGGTCG
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-08-26
PRIOR PILING DATE: 2000-08-26
PRIOR PILING DATE: 2000-08-26
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
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FILING DATE: 2000-09-21
PAPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
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US-09-864-761-19241
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1051 AGAAGCAGCGGGGGCAGCGGGGGGGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGG 1110
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                                                                                                                                                                                                                                                               Length 1030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 7.1e-09;
0; Mismatches 186;
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CURRENT PPLICARION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
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COGANISM: Glycine max
US-09-371-307-5
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Matches 19
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                                                                                       TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REPERBURE: Asomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23
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N: EXPRESSED IN BONE MARROW, SIGNAL = 27

N: EXPRESSED IN LUNG, SIGNAL = 19

N: EXPRESSED IN BT474, SIGNAL = 34

N: EXPRESSED IN BT474, SIGNAL = 34

N: EXPRESSED IN METAL LIVER, SIGNAL = 7.1

N: EXPRESSED IN HELA, SIGNAL = 43

N: EXPRESSED IN HELA, SIGNAL = 20

N: EXPRESSED IN HELA, SIGNAL = 25

N: EXPRESSED IN HEARY, SIGNAL = 25

N: EXPRESSED IN HEARY, SIGNAL = 18

N: EXPRESSED IN HEARY, SIGNAL = 18

N: EXPRESSED IN HEARY, SIGNAL = 18
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 2513
                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-08-03
PRIOR PLICATION NUMBER: US 60/236, 359
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00668
                         Rank, David R.
Hanzel, David K.
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                                                                         Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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OTHER INFORMATION:
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CTTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGGCTGGAGA 1174
                                                                                                                             TGAAGAGGCGAGGAGGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCGCGCAGCACGG 1234
                                                                                                                                                                                                                   1235 GCGGCGGCTGGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGGCTGTCGCTGGA 1294
                                                                                                                                                                                                                                              451 GGTGCAGGTGCAGCAGCAGCAGCAGCAGCCGGAGGTGCTGGACAAGGAGATACGGTGGT 510
                                                                                 CITCGTGGACAAGGTGCCGGACAAGGTGGCTATGGAGGATTGGAAGCCAAGGTGCCGGA
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Sequence 4, Application US/09969852

Patent No. US20020137211A1

GENERAL INFORMATION:

APPLICANT: Liu, Hinfen

APPLICANT: Liu, Hinfen

APPLICANT: Liu, Heilen

APPLICANT: Liu, Heilen

TITLE OF INVENTION: GENE IN BOMBYX MORI

TITLE OF INVENTION: A METHOD FOR ESTABLISHING AN EXPRESSION SYSTEM OF SPIDER DRAGLINE

TITLE OF INVENTION: GENE IN BOMBYX MORI

TITLE OF INVENTION NUMBER: US/09/969,852

CURRENT FILING DATE: 2001-10-04

PRIOR FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 14

SOSTWARE PATENTIN VERSION 3.1
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                                                                                                                               1559 GETCGGCGACACCTICATGGCGCTCTCCAACGCCAGGTACCGCAGCTGCCTGCACCGGGC 1618
                                                                                                                                                                                                                     .619 GGTCGTCAACAGCACGCGCCTCGCCGCTCGCTGGCCTTCTTCCTCTGCCCGGAGATGGA 1678
                                                                                                                                                                                                                                                                                                          CACGGTGCTGCTCCCCCCCCGGAGGAGCTCGACGACCACCACCCGGAGGGTGTACCCGGA 1738
                                             1502 GT---GGGCGGAGGGGCGGTGGCGCCCATCCGCCTCGCCCCGGGGCGCTCGTCAA 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCCTGATCGACGTGGGGGGGGGGGGGGAGAGGTCGTCGGTGGTCCGGCAGGTGGGGGA 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 CGAGGIGGATCAGGIGGACAAGGGGCAGGIGCAGCAGCAGCAGCAGCIGGAGGIGCCGGA 390
                                                                                                                                                                                                                                                 761 GCAGGAGCAGGAGGTGGTGTTCGACGCGCGGTGCTGAGCGGGCAGACGGAGATCCCGTC 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGTTCATATGGCCGCCGCAGGAGAGACCCCCGGGTCGGTGGCGGTGGAGGAGCTGGAGGT 880
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                                                                                      735 TCACCGAAAAGGCGGGGGGGGGGGGGGGGGCACCAGTCCCCGAAGGGCTTGTGATCAA 794
                                                                                                                                                                          795 TETAGGCGACCTCCTCCACATATTGTCGAACGGGTTGTACCCGAGTGTGCTCCACCGGGT 854
                                                                                                                                                                                                                                                                                                                                   Gaps
  675 CCACACCGACTCCACCTTCTCACAATCCTTTACCAAAACAACATAAGCGGGTTGCAGGT 734
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                                                                                                                                                                                                                                                                                                                                                                                              1739 CTTCACGTGGCGGGCGCTGCTGGAC 1763
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Matches 271; Conservative
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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March 26, 2003, 04:18:30 ; Search time 9640.7 Seconds
(without alignments)
15096.740 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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5001
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                                                                                            Run on:
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REFERENCE AUTHORS

is the number of results predicted by chance to have a

Pred. No.

ncusovy Oryza sativa chromosome 3 clone OSJNBa0059G06, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces. APO104117 Oryza sat AP0104413 Oryza sat AP010459 Oryza sat AP010459 Oryza sat AP0104130 Oryza sat AP0104130 Oryza sat AP010414 Oryza sat AP010419 Oryza sat AP010419 Oryza sat AP010419 Oryza sat AP010415 Oryza sat AP010415 Oryza sat AP010410 Oryza sat HTGS. HTGS. PHASE2.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 145999)

Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K., AC096690 Oryza sat AC104433 Oryza sat AC104433 Oryza sat AP005459 Oryza sz AL662957 Oryza sz AC093088 Oryza sz AP003984 Oryza s AP005535 Oryza s AL606620 Oryza s AL731619 Oryza s AP002092 Oryza s AP004564 Oryza s AP004764 Oryza AP005459 Oryza ALIGNMENTS AC120534 OSJN01010 AP003634 OSJN00065 OSJN00267 AP002092 AP003579 AP004809 AP005449 AP003712 AP004156 AP004991 AP004849 AP003952 AC096690.4 GI:20503077 DB 100.0 145999 40.7 207376 18.8 207376 6.3 131487 5.5 159290 5.3 96360 55.3 56.3 64.6 61.274787 64.6 61.2759 64.6 61.2759 64.3 10.2759 64.3 1 4.1 176580 4.1 130263 4.0 114062 4.0 176349 Length 144583 5001 938.8 315.2 274.8 263 263 261.4 231.8 215.4 215.4 215.4 215.4 215.4 RESULT 1 AC096690/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION Result No. U

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Kim, M., Overton II, L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B.,
Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.,
Utterbach, T., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J.,
Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0059606 BAC genomic
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* This sequence will be replaced.

* This sequence will be replaced.

* By the finished sequence as soon as it is available and the accession number will be preserved.

* 3902 contig of 3902 bp in length

* 4003 71267: contig of 67265 bp in length

* 71268 71367: gap of unknown length

* 71369 94779: gap of unknown length

* 94680 94779: gap of unknown length

* 94789 122221 contig of 27441 bp in length

* 122221 122320: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TGAATATGAAGTTGTACTGGGCTAAATTGGAAATTTAATTATACCAAGCCAATTCA 120
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                                                                                                                                                        2 (bases 1 to 145999)
Buell, R.
Direct Submission
Submitted (22-SEP-2001) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                           Submitted (08-MAY-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA On May 8, 2002 this sequence version replaced gi:19881893.
* NOTE: This is a "working draft' sequence. It currently
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Direct Submission

Submitted (02-APR-2002) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

On Mar 5, 2002 this sequence version replaced gi:18767486.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 34 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Direct Submission
Direct Submitted (11-DEC-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 207376)
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/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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/clone="0J1754_E06"
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                                                          CCGTGATAATCACCTTATACCAGTCAAGAATGACTTGCCTATGCACAATGAAGAGGAGCA
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1 (bases 10 207376)
Buell,C.R., Yaban,C., OuyanquS., Liu,J., Tallon,L., Gansberger,K., Kim,M., Overton II.L., Bera,J., Tsitrin,T., Krol,M., Jarrahi,B., Jin,S., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S., Utterbach,T., Reldblyum,T., Yanq,Q., Haas,B., Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and Fraser,C.
Ourza sativa ssp. japonica cv. Nipponbare OJI754_B06 BAC genomic
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Medical Center Dr. Nockville, MD 20850, USA.

On Mar 5, 2002 this sequence version replaced gi:18767486.

* NOTE: This is a 'working draft' sequence. It currently.

* consists of 34 contage. The true order of the pieces.

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
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HTG 21-MAR-2002
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Direct Submission
Submitted (29-AuG-2011) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakieilas.affrc.go.jp, VRL:http://rgp.dna.affrc.go.jp/,
Tel.31-296-38-7444, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 167706 ACAATGGAATTATTTTGGCATGTCTACCTGACGGAATGTGATGGTATGTTATATA. 167765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 167766 GGAGAAGACCAGAACCAGACCAGACCAGACAAATAAGTAGCTTGGAATATAAGTATGTTGG 167825
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 167406 TAGCAGCGAAGAGTCTAATTTACAAGCGATTGACGAAAAACCACAAATAGTTTGTCTTG 167465
                                                                                                                                                                                                                                                           DD 167466 CATTGCCTGGGTGGTTTGAATGAGGAGAAAAAATGCAATGGTCCATAGTAAGATGACAG 167525
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CTAAGGTGCAGATGGCCATCTTCTAGTGGCAAACCCTTTGCATCAAAAATCTCACGTTT 360
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OJ1134_F06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP004117
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                                                                                                                                                                                                                                                                                                                  ACAATGGAATTTATTTGGCATGTCTACCTGACGGAATGTGATGGTATGTTATTACATTA
                                                                          421 GCTAGTCCTACCTGAAACACCAAACAGGAATGGGGATTGCCTACTGTATTATGTGATA
                                                                                                                                                                                481 TAGCAGCGAAGAGTCTAATTTACAAGCGATTTGACGAATACCACAAATAGTTTTGTCTTG
                                                                                                                                                                                                                                         541 CATTGCCTGGGTGGTTTGAATGAGGAGAAGAATATGCAATGGTCCATAGTAAGATGACAG
                                                                                                                                                                                                                                                                                                    601 TAGTIGIGCAIGTAGACCTIGGACAIATAIATGCCTAITCTAIACAGAIATAIATAGGGA
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                                                            CGAAGITTGATCCCTTTCTGAGCTTCCCTTACTACTTCAGTATATTGCCCCAAGCCCTGAT
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
clone:031134_F06
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HTG; HTGS_PHASE2.
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combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3458 AACAAGAGCA--GGCAGCACAGGCCGGAGGAACAITGTGAATAGAGGACTGCACGAGCAC 3515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3516 CGGAGCACGCGAGTGGGTTACGAGCGCGCGCGCGGGGGTGCACGGCCGACGGGACGG 3575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------GUTGTCGCCCTGTCTTCTGTGTTCTCCCCCGCCATTCGCC 3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TCCCATCAATCCGCGTAATCTCG 3719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3720 CCGCCGGTGCCCCAATTTGC------CTCAAGCTCTTCCAAGCCGCCCCCT 3765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3766 CCAGGAATTGCAGCGTCGGTCAACATCGTGCTCTCCCGCGCCCAA-CCCCTTCCTCACACA 3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3219 TITALACCATCGAAAATTTGTGGTGCACTTTAATACCATTCAAAGTTTTCTCCGTTAACT 3278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3279 CICIATACCACACIGITTATITICCGICAGITT-TITITICITITICATATITIGGCIGGA 3337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3338 AGACAAACAGGATATGACTGTATTGCCCTTCCTTCACTCTAAATCTGGCCCAAATT 3397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGGATGGCTG-GCCACCTCCGACAGGTGCGGTGGCAAGAGGATGTGATGGAGCTGGCGG 3883
                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3619 AATCTACACGTCCCTGCTACTGATCTCTTCCCTACCGGTGAGCTGGTCCCCACCATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44771 resrescescentrisceceaetrrassescassesascescescescescescesces
                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 131487;
                                                                                                                                                                                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                                                                                                                                                       others
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                       Score 315.2; DB 2;
Pred. No. 2.4e-42;
0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                  /clone="0J1134_F06"
26762 c 26756 g 39195 t
                                                                                                                                                                                                                                                            /cultivar="Nipponbare"
                                                                                                                                                                                                                                                                             /db_xref="taxon:39947"
                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                  /chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                         6.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
1; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza satīva (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0459E03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 27070 GGCAGTGGGCGGCTGGAAAGGGGGGGAGAGGCGGCCGTGAGCCTGGGAGGAGGAGAGG 27011
                                       --- ATGCGTCGGGGACCCGAGACAAGG 44977
                                                                                                1504 GTGCGGTTGGAGTCGATGCCGTTGTGGAGCGCCTCGTGGGCCTCCTCCCATCGGAGCTGC 1563
3884 CGATGCTTGGTGAAGAAGATGCTGCTTTTGATCTGGATGCGTCGGGGGACCGGAGAAGG 3943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1444 GGGAACTGGCCGGAGCGAAGGAGGCCTTAGCGAAGGACATCCCGGGACCGCCGCACGCCGCAG 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1564 GGGGAGAGGCGGAGGATGGAGGGTTGGGGGCGCACTCCGGG-GGAACCATGCCGTCCCA 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
                                                                             3944 GCAAGCAATGTCATGTTTAACGACAGATCCACTAAAGTTGACGGTGATGGTGAAATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 159290;
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:P0459E03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantaes; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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/db_xref="taxon:39947"
/chromosome="6"
                                                                                                                                                                                                                                                                                                159290 bp
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1. .159290
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                                                                                                                                                                                                                                                                                                                                                                               GI:19223840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.5
Best Local Similarity 79.0
Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                             AP004813,1 GI:1:
HTG; HTGS_PHASE2
                                                                                                                                                                                                45038 CCCGGTTTGATT 45049
                                                                                                                                                          4004 AACGGAGTAAAT 4015
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HTG 05-JUL-2002
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OSJUBA0049101, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza satīva (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBa0049101.
                                                                                                                                                                                                                                                                                                               98009
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                                                                                                                      2351 ACCTAGGTGTCTGGGCACCAAGCCTGATACTTGTGGTTATCGGGCTGTGATTTTCTGACGT 2410
                                                                                           Gaps
                                                                                                                                                                                               -----AATGACTTGCCTATGCACAAGAGGAGCAGCATGACGAGCTAGCGACA
                                                                                                                                                                                                                                                                    60320 TACTAGTCTAGTAACTTACCTACCTATAATGAAGAGGAGCACACAACGAGCTAGCGAGG
                                                                                                                                                                                                                                                                                                                                                         2574 GACCGAC-----TIGCTITTAICCTITGGIGCCCTITGACCTCATCTCCCTCAGCCTCGC
                                                                                                                                                                                                                                                                                                                                                                          ||||| || GACCAACTATGCATTGTCCGTTGGTGCCCCTGACCTCATCCCCCTTTCCCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCTCCTCTTCTCCCTCCCCAGCCACGCAAATGGCAAACCTCACCACCGCAGTAACCT
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                                                                                                                                                                                                                                                                                                AGTACAATGTAACAACCTCGAGACCTCCATGAACTCCGAGATTGCCCTCACACGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCTCCCTCTTGTCCCTCCCCAGCCACGACAATGGTGACCTCGCTGTCGCAGTTACCT
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Oryza sativa (japonica cultivar-group)
Bukaryota; Vitidiplantas; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae;
                                                                                         50;
                                                         Length 96360;
                                                                                                                                                                               2411 ACCAGGCCTAATACTTGGTATCAGCCGTGATAATCACCTTATACCAGTCAAG-
                  200 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                         Indels
                                                                                         0; Mismatches 160;
                                                            Score 263; DB 2;
Pred. No. 1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
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                  27049 t
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 /clone="OJ1111_B02"
21675 c 21926 g
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                                                            5.3%;
                                                                           69.1%;
                                                                                         Matches 469; Conservative
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                                                                          Similarity
                  25510 a
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                                                             Query Match
                                                                             Local
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                  SASE COUNT
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AP005490
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SOURCE
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                                ORIGIN
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                              26724 ATAATCAAGCAAATTIGAAATCTACTCTTCCT----CCCTACTCGTAGTCAATTTATAC 26670
                                                                                                                                                                                                                                                                                              Oryga satīva (japonica cultivar-group) (cultivar:Nipponbare) DNA clone:OJ1111_B02,
26890 GIGGGAICCCACCACGCCGCGCGCCACGAIGTICGACIGCCCGGCCAGGAIGAACAC 26831
                                                                                                       1742
                                                                                                                                                             1743 CAGCAGCATCGCCGCCATTGCTGCTACCGTTGGGCCTTGGGGGCGCTTGGGGGGGTTGGGT 1802
                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) chromosome 8 clone
OJ1111_B02, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP003867
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
clone:OJ1111_B02
Published Only in Database (2001)
2 (bases 1 to 96360)
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                                                                                                       GIGGGACCCCACCACCCCCCCCCCCCCCCCCATGIICGACTGCCCCCCCAGGAIGAACAC
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Direct Submission
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/db_xref="taxon:39947"
/chromosome="8"
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Submitted (13-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-6602, Japan 12-1-2, Tsukuba, Ibaraki 305-6602, Japan 12-1-2, Tsukuba, Ibaraki 305-6602, Japan 12-1-3, Tsukuba, Ibaraki 305-6602, Japan 12-1-308-38-7441, Fax:al-296-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are peptesented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                     AP004759 127498 bp DNA linear HTG 21-MAR-2002 Oryza sativa (japonica cultivar-group) chromosome 8 clone P0670E08, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
  -----AGTIGGGGGAGGGAGCAAGGIGGAGGAIGGAGAAIGAGIITGAGAAAAGG 134246
                                                                                   Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0670E08.
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    1. 127498
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"

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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
clone:P0670E08
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2 (bases 1 to 127498)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
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                                                                                                                           Direct Submission
Submitted (04-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1.2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakianias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:181-298-38-74468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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/cultivar="Nipponbare"
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
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Pred. No. 1.2e-33;
                                                                                                    Sasaki, T., Matsumoto, T. and Katayose, Y.
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              * is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 3902: contig of 3902 bp in length
* 4003 71267: contig of 67265 bp in length
* 71268 71367: gap of unknown length
* 71368 71367: gap of unknown length
* 94680 94779: gap of unknown length
* 12222: contig of 23312 bp in length
* 12222: contig of 2341 bp in length
* 12232: contig of 23679 bp in length
* 12232: Location/Qualifiers
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are represented as runs of N. The order of the pieces
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0; Mismatches 192;
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/organism="Oryza sativa"
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Matches 385; Conservative
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1 (basea 1 to 14599)
Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K., Kim,M., Overton II,L., Bera,J., Tsitrin,T., Krol,M., Jarrahi,B., Jin,S., Koo,H., Zismann,Y., Hsiao,J., Bulut,S., Yanaken,S., Utterbach,T., Feldblyum,T., Hang,D., Salb,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and Fraser,C.
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Oryza sativa chromosome 3 clone OSJNBa0059G06, *** SEQUENCING IN
PROGRESS ***, 5 ordered pieces.
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                                        77201 GACCAACTATGCATTACCATTGTCGTTGCTGCCCTGACCTCATCCCCCTTTCCCTGAC 77260
                2514 AGTACAATGTAACAACCTCGAGACCTCCATGAACTCCGAGATTGCCCTCACACGAGAAC 2573
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On May 8, 2002 this sequence version replaced gi:19881803.
* NOTE: This is a "working draft" sequence. It currently
* consists of 5 contigs. Gaps between the contigs
                                                                                                                                                                                                                      2574 GACCGAC-----TIGCTTTTATCCTIGGTGCCCTTGACCTCATCTCCCTCAGCCTCGC
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Direct Submission
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Submitted (1976a7202) land) land)
Agrobiological Sciences, Rice Genome Research Program: Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tisasakienisas.affro.go.jp, NEL:http://rgp.dna.affro.go.jp/, Tel:181-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is a the accession number will be preserved.

* the accession number will be preserved.
                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Bukaryota, Vinidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Oryza.
                                                                                                                                                                                              Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBaC053M06.
                                                                      Oryza sativa (japonica cultivar-group) chromosome 8 clone
OSJNBa0053M06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46774 TACTACTCCCTCCGTTCCAAATAAGTGTAGTTTTAGCACTGTTCATGTTCAAGGTTTGA 46833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-MAY-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                        Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
clone:0SJNBa0053W06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 176224;
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                                                    linear
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Pred. No. 2.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki,T., Matsumoto,T. and Katayose,Y. Direct Submission
                                                    DNA
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2 (bases 1 to 176224)
                                               176224 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="8"
                                                                                                                                                  AP005163.1 GI:20975289
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%;
Local Similarity 94.1%;
ies 240; Conservative (
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                                                    AP005163
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REFERENCE
  RESULT 11
AP005163
                                                                                                                          ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-SEP-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-12, Tsukuba, Ibaraki 305-8602, Japan 12-12, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@idas.affrc.go.jp, URI:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nuclectide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                    APO04130 121752 bp DNA linear HTG 21-MAR-2002 Oryza sativa (japonica cultivar-group) chromosome 8 clone OJ1014_B05, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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                                                                                                                                                                       Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:031014_B05.
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiphantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95625 TACTACTCCCTCCGTTCCAAAATAAGTGTAGTTTTAGCACTGTTCATGTTCAACGTTTGA 95684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95745 ACATGAATAGTAATTTATGTGTGACTAATTTTTTTTAATATTTTTCATAAATTTTTTCAA 95804
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/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                              8, BAC
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:0J1014_B05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the accession number will be preserved. Location/Qualifiers
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Pred. No. 2.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                          Published Only in Database (2001)
2 (bases 1 to 121752)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
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32506 a 27609 c 27315 g 34122 t
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                                                                                                                                                                                                                                                                                                    Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                          GI:15451451
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94.18;
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                                                                                                                                                  HTG; HTGS_PHASE2
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Best Local Similarity
                                                                                                                          AP004130.1
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RESULT 12

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KNIYKVISJILIGVGLILINOSTSVGBICVCKYKKEKTHPAYKETHLDITEMIDIIKVIRM
KNYKVISJILIGVGLILINOSTSVGBICVCKYKKEKTHPAYKETHLRPIRRKYTDWRA
HKSODATERVITVITAIRANGSVSLEPKERLGDLSEVDGRLSNKPNMLEKLNIADLHQ
WYNAVHITTRYNYTERIKKRIFVSG"

join (24567. 24773,24885. 25163,25427. 25524,25675. 25882)
/gene="Billibil.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(24567. .24773,24885. .25163,25427. .25524,25675. .25882)
gene="B1111B11.5"
         /translation="MTSPPAVARARKLASERRRDDANGGHQHINGRRRRGRNGGNLR
.DDDGGAPATYGDGGGVDEIGDGLVTTTATSPSNDDDRTDGGARLKLRRRRRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKTWASRTLREFAAPSADNVATRLOFLEICSTYTIKGVNLDAVRLRLFLFSLLGRAKQ
WFYINRVAVNTWDKCSTAFLSKFFPMGKINALRGRISSFQTRDESIPBAWERLQEYG
WKTIEESRAGGIYRETRNMTRNERESSSSSTPVQMSSGVPPSPSEGWRSSSSRWDLSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mplfclkkvkkkonmipghigyigcvpgknslrdshgelpsina
nigtrgcdvfdrngkagkmpkhdpwtywsmlrafvakthfviraanfcgliatlaheg
amffdrnekvgkapkgdfwtywsvkertafrtpgddreprpenlrndrsyakhtskat
                                                                                                                                                                                                                                                                                                                      /translation="MEDHTRKLQNKADIASAEVHKSGGWGTDEQAVIGYLAHRDATQR
KQIRLTYEENYNENLIQRLQSELSGDLERAMYHWYLDPVERQAVMVNTATKCIHEDYA
                                                                                                                                                                                                                                                                                                                                                                                     VNDALAKSEAKILHETVTNGDTDHGELIRIVGTRSRAQLNATFSWFRDERGTSITKLH
APRFDHQALQHGADPTGYSHALRTALRCISDANKYFVKVLRNAMHKSGTNEDSLTRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(17303. .17441,21169. .21190,21797. .22025,
22151. .22324))
/gene="B1111E11.4"
                                                                                                                                                                                                                                                                                                                                                                VIVEIACTNSSSELLAVKRTYHVLYKCSLEEDVAARATGNLRSLLLALVSTYRYDGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTGFNLSENFKENPEAFFRSVRPRVVAPKKSLPIEKLAIPVPPT
                                                                                                                                                complement(join(14589. 14792,14904. 15023,15078. 15290,
15389. 15607,15720. 15865,16296. 16365))
/gene="BilliEil.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                  VLHAEKDLKGIKDAFQKRASVALEKAIGNDTSGDYKSFLMALLGSGI"
complement(join(17303. 17441,21169. 21190,21797. .22025,
                                                                                               .15023,15078. .15290,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein
similar to Oryza sativa chromosome10,0SJNBb0089F16.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30135. .3223
/gene="B1111E11.6"
30135. .32223
/gene="B1111E11.6"
/note="probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein similar to Oryza sativa chromosome3,OSJNBa0026A15.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRRMDTLDIQIGEIQYNLTEHVAQTQEWQQSADAQFANINDMMQQ"
                                                                                        complement(join(14589, .14792,14904, .15023,
15389, .15607,15720, .15865,16296, .16365))
/gene="BilliEil.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(35262. 35643,43596. .43702)
/gene="ballibil" 7"
join(35262. .35643,43596. .43702)
/gene="ballibil" 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
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                                                                                                                                                                                                                                                       /product="putative annexin"
/protein_id="BAC03328.1"
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/gene="B1111E11.8"
join(44530. .44843,44934.
/gene="B1111E11.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAC0330.1"
/db_xref="G1:21743337"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAC03329.1"
/db_xref="G1;21743336"
                                                   complement(8839. .9352)
                                                                                                                                                                                                                                                                                                   /db_xref="GI:21743335"
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/gene="B1111E11.4"
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                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
       aruo4224 152835 bp DNA linear PLN 13-JUL-200
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
BAC, clone:B1111E11.
                                                                                                                                                       Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:B1111F11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"probably inactive due to stop codon(s) in CDS pseudogene, polyprotein"
                                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:B1111E11
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.cultivar="Nipponare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeg.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
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Join(8253. 8336,8386. 8595)

/gene="B1111E11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAC03327.1"
/db_xref="GI:21743334"
                                                                                                                                                                                                                                                                                                                                                                                 Published Only in Database (2001)
2 (bases 1 to 152835)
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/gene="B1111E11.1"
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/gene="B1111E11.1"
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                                                                                                                                                                                                                                                                          Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1. .514)
/note="3' LTR"
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                                                                                                             AP004224.3 GI:21743333
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Agrobiological Sciences, Race Genome Research Program; Kannondal 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasakiénisa.affrc.go.jp, URL; http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-37468)

The nucleotide sequence of this BAC clone was generated by combining Monsauto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:011311_D08.
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4129 AATAGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAACGTTT 4188
                                                                                                                                                                                                                                    AP004849 163704 bp DNA linear HTG 23-MAR Oryza sativa (japonica cultivar-group) chromosome 2 clone OJ1311_D08, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Direct Submission
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:011311_D08

    163704
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                DD 78393 CGGAGGTAGTATCACCTTAGCTCCCACCAAATAAGATCTAAACTTATCGAA 78443
                                                                       4369 CGGAGGTAGTAGGCTATAAACCAGCTATAAACATATTTTAAAGAGATAAAA 4419
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Pred. No. 6.3e-26;
0; Mismatches 19;
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35204 c 34892 g 46875 t
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                                                                                                                                                                                                                                                                                                                                GI:19698269
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HTG; HTGS_P
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//gene="Billibill2"
join(60720. .61097,61272. .61421,62316. .62685,62854. .62971,63377. .63182,63282. .63374,63454. .63549,64125. .64847,796ne="Billibill1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BaC0334.1"
/db_xref="GI:21743341"
/translation="MLRALPEKYETLVTMLINSDMSRWTPASLLGKINTNDMYKLKKK
EMEEASPSKPKLKIRARAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ĥ
                                                                   /translation="mrrgsrqqlhggedgaehaanpTypaaprddeparrngrpee
gaayegddddehraggggearaytllkgryrwyrgrrngggradbgnbeyrg
wpsggdayghrwatsgglrakrrrwyrkrrgyfdyceaegggddyshyghadgaapapagaegp
prkekeeygrggaatenlgrglkrenarrgffigeerelatgeaggggdrarpw
                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTGFNLPENFKEYPEAFFRGYRPRAVAPQKTLPTEKPAIPAPPI
FNTMASKTLREFAAPSTDNVAIGPQINIGDMDFDLKSSLITMAQASPFCGKPNVDANA
HLQQFLEICSTYTIKGVSPDAIRLRLFPFSLLGRAKQWFYANRAAVNTWDKCSPGFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similar to Arabidopsis thaliana chromosome 3, At3g54500"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4129 AATAGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAAGGTTT 4188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFFPMGKTNALRGRISNFQQTRDESIPEALERLQBIYAACPHHGMDDWLIVTS"
complement(48388. .48579)
gene="B1111E11.10"
complement(48388. .48579)
/gene="B1111E11.10"
                                                                                                                                                                                                                                                                                                            similar to Oryza sativa chromosome10,0SJNBb0089F16.9"
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                                                                                                                                                              VAGVGAGVPDDWGHESRGKLGGIEEBEGMGINSP"
complement(46012. ,46653)
fgne="B1111E11.9"
complement(46012. ,46653)
/gene="B1111E11.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAC03335.1"
/db_xref="GI:21743342"
                   /protein_id="BAC03332.1"
/db_xref="G1;21743339"
                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAC03333.1"
/db_xref="GI:21743340"
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/note="5' LTR"
55770. 57516
/gene="B1111E11.11"
/gene="B1111E11.11"
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Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tessaskiehisas.affro.go.jp, WEL;http://rgp.dna.affro.go.jp/, Par.ail:tessaskiehisas.affro.go.jp, WEL;http://rgp.dna.affro.go.jp/, Par.ail:tessaskiehisas.affro.go.jp, WEL;http://rgp.dna.affro.go.jp/, Tel:81-298-38-7441, Fax:81-289-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Embryophyta; Tracheophyta;
1; Poales; Poaceae;
Db 113730 ATAAGACGGATGGTCAAAGCGCTAAATIACGGATATTTATGGCTGCACTTATTTGGGACG 113789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:031147_D11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4177 IGITCAACGITIGACCAIRCGICITAITIGAAAAAGAITAIGAITAGIAITITIAIIGI 4236
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                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) chromosome 6 clone
0J1147_D11, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC clone:OJ147_D11
Published Only in Database (2001)
2 (bases 1 to 138906)
Sasaki, Y. Matsumoto, T. and Yamamoto, K.
Subnisted A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-JUL-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
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Eukaryota, Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Lillopsida;
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39967 a 29996 c 29997 g 38791 t
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1. .138906
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Oryza sativa chromosome 3 clone 031263H11, *** SEQUENCING IN
PROGRESS ***, 3 ordered pieces.
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Oryza sativa.

Oryza sativa.

Oryza sativa

Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Varidiplantae, Oryzae; Uliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 126637)

Wing, R.A., Tu.Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T., Saski, C., Hory, D., Oates, R. and Simmons, J.
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4309 AAAIAAGACGGAIGGICAAAGCGCIAAACAIGGAIAICIAIGGCIACACIIAITIIIGGGA 4368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-APR-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. Gaps between the configs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Direct Submission
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

I 19607: contig of 19607 bp in length of the continue of the
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/organism="Oryza sativa"
/db_xref="taxon:4530"
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AC118980.1 GI:20270052
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Search completed: March 26, 2003, 16:07:03 Job time: 16632.4 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC Gaport 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                             Run on:
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Description	Rice Ditto-Osl nuc	Rice Ditto-Os1 nuc	Nucleotide sequenc	Rice Ditto-Osl nuc	Nucleotide sequenc	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia
SUMMARIES ID	ABL49988	ABL49989	AAZ61434	ABL49987	AAZ61433	AAC48061	ABN98574	AAC45528	AAC46278
DB	24	24	21	24	21	21	24	21	21
% Query re Match Length DB	561	261	5113	544	5757	2943	949	1024	3108
% Query Match	2.8	2.8	2.7	2.6	2.4	2.4	2.4	2.4	2.4
Score	139.8	139.8	137.4	129.8	121.8	118.8	118.4	118.4	118.4
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0	13	107.8	7	2380	201	AAX32000	Rice pyruvate deca
O	14	107.8	?	5526	20	AAX31999	Rice pyruvate deca
C	נה ה	66	0,0	15686	27.0	AAD38801	Rice RGA38 contig.
ບເ	1 P	4, 1,	να	1730	4 C	AAL46938 AAT72980	Atce resion innibit
υO	18 18	91.6	, ω	3572	24	AAI72979	OsGRP-Al coding se
ပ	13	9.68	œ	267	24	ABL49990	Rice Ditto-Os2 nuc
O	20	84.2	٠. ١	312	24	ABL49992	Rice Ditto-Os2 nuc
υ (77	83.4	- 4	246	4.5	ABL49991	Rice Ditto-Os2 nuc
נ	7 K	73.2	. ₁₂	1026	50.4	AAX33542	Rice beta-qlucanas
	24	73.2	ı,	2169	20	AAX33534	Rice beta-glucanas
O	25	9.69	₹.	91552	24	AAD38803	BAC clone K6P36 fr
	56	65.4	m, i	18155	24	AAD38808	CODR4 ORF from ric
	27	65.4	m, c	91552	77.	AAD38803	BAC clone K6P36 Ir
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י כ	3 6	62		1806	1 (-	AAA50102	Human Znfr2 consen
•	32	62	. 7	12120	24	AAS96695	Rice DMT1 DNA. Or
O	33	62	3	125401	22	AAD17186	Streptomyces nours
· O	34	61.6	3	65140	22	AAD17184	Streptomyces nours
	32	61.2	7	1050	22	AAD21685	Mutational hot spo
	36	61.2	7	2849	22	AAD21684	Human retinitis pi
	37	61	ď	863	24	ABK77958	Bacillus clausii g
ပ	38	61	?	4403765	22	AA199683	Mycobacterium tube
	99	61	7	4411529	525	AA199682	Mycobacterium tube
	40	60.6	7.	1280	7.	ABQ62495	Mycobacterium bovi
ပ	41	9.09	. i	15872	8 6	AAT68715	Streptomyces venez
O	4 4	9.09	4 0	158/2	4 o	AA28/283	S. Venezuelae Vep
	4, 4 A) 4	. 0		1001	2 0	AAT93/8U	Dandomicing paulic
	44	09	1.2	390	14	AAQ21833 AAQ36859	PCR primer for 5'
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RES	RESULT 1						
ABL4	49988						
A	ABL	19988	standard;	DNA;	561	BP.	
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AA PF	02-	02-AUG-2001;		2001WO-JP06661	661.		
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PR	.03-	-AUG-2000;	2000JP	JP-0234577	577.		
PA PA	(NISB	~~		TOBACCO INC	ပ်		
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V Ed	Con	struction	of	marker f	for d	etecting plant genome po	olymorphism with use
E A	of	of transposable	ole ole	u		eful particularly in studying restriction	lying restriction

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                                                                                                Also described is a marker for detection polymorphisms in plant genomes. The constructed marker can be used for detecting plant genome polymorphisms, which is useful particularly in studying restriction fragment length polymorphism applicable in cell genetics e.g. for analysing and selecting specific breeds of plants. The method is simple, easy, less time consuming and not so laborious, e.g. in the study of less frequently occurring polymorphism between various species to enable identification of the site and isolation of the required gene.

ABLA9926 to ABLSO036 represent nucleotide sequences used in the exemplification of the present invention.
                                                           detecting polymorphisms in a plant genome. The method comprises the production of a primer for nucleic acid amplification by using the base sequences of a transposable element and/or the domain adjacent to it.
                                                  present invention describes a method for constructing a marker for
                                                                                                                                                                                                                                                                                                                                                                                                                      4495 IGACAAGTAGGACCAGGTATTAAGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTA 4554
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                                                                                                                                                                                                                                                                                                                    4435 CAGCGGACTATATTTGTAGCCAGCTACAGCACGACTCAAAGACGTAATGTGTGTATA 4494
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                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                  2.8%; Score 139.8; DB 24; Length 561; ilarity 75.9%; Pred. No. 4e-20; Conservative 0; Mismatches 57; Indels 2;
                                                                                                                                                                                                                                                                                           57; Indels
fragment length polymorphism applicable in cell genetics
                                                                                                                                                                                                                                         Sequence 561 BP; 191 A; 76 C; 87 G; 207 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice Ditto-Os1 nucleotide sequence SEQ ID NO:64.
                       Example 4; Fig 17; 110pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL49989 standard; DNA; 561 BP
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                                                                                                                                                                                                                                                                               Local Similarity
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detecting polymorphisms in a plant genome. The method comprises the production of a primer for nucleic acid amplification by using the base sequences of a transposable element and/or the domain adjacent to it. Also described is a marker for detection polymorphisms in plant genomes. The constructed marker can be used for detecting plant genome polymorphisms, which is useful particularly in studying restriction fragment length polymorphism applicable in cell genetics e.g. for analysing and selecting specific breeds of plants. The method is simple, easy, less time consuming and not so laborious, e.g. in the study of less frequently occurring polymorphism between various species to enable identification of the site and isolation of the required gene.

ABL49926 to ABL50036 represent nucleotide sequences used in the exemplification of the present invention.
                                                   Construction of marker for detecting plant genome polymorphism with use of transposable element, useful particularly in studying restriction fragment length polymorphism applicable in cell genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for constructing a marker for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4495 TGACAAGTAGGACCAGGTATTAAGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTA 4554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 TGATAGGTGGAACCAGGTATTAATAGTACAGTAAGCAACTATTGTATGAATTGACTATTA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease resistance protein; rice; variety Tsuyuake; Pi-ta gene; resistance gene; Pi-ta resistance gene-mediated defence response; fungal pathogen; rice blast fungus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24; Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of the genomic clone of the Pi-Ta gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4e-20;
0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 561 BP; 191 A; 76 C; 87 G; 207 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 139.8; 75.9%; Pred. No. 4e-2
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                                                                                                                                                     Example 4; Fig 17; 110pp; Japanese.
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Matches 186; Conservative
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WPI; 2002-241759/29.
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The present invention describes a method for constructing a marker for detecting polymorphisms in a plant genome. The method comprises the production of a primer for nucleic acid amplification by using the base sequences of a transposable element and/or the domain adjacent to it.

Also described is a marker for detection polymorphisms in plant genomes. The constructed marker can be used for detecting plant genome.

The constructed marker can be used for detecting plant genome polymorphisms, which is useful particularly in studying restriction ranging and selecting specific breeds of plants. The method is simple, easy, less time consuming and not so laborious, e.g. in the study of less frequently occurring polymorphism between various species to enable identification of the site and isolation of the required gene.

Abidagoze to AbiSol036 represent invention.

Exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4445 TATATITGTAGCCAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATATGACAAGTAG 4504
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                                                                                                                                                                                                                                                                                                                                                                                                            Construction of marker for detecting plant genome polymorphism with u of transposable element, useful particularly in studying restriction fragment length polymorphism applicable in cell genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 AGATGATTTTAAGTTAGTAGTGGGCTATACTATTAAACTTGCTCTAATTGTTTTA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24; Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of the genomic clone of the Pi-Ta gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.6%; Score 129.8; 74.9%; Pred. No. 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig 17; 110pp; Japanese
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                                                                                                                                                                                                                                                                (NISB ) JAPAN TOBACCO INC (SYGN ) SYNGENTA LTD.
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Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-241759/29.
                                                                                                                                                                                                                                                                                                                            Komori T, Nitta N;
                                                                                                      WO200212484-A1
                                                              Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid fragments conferring Pi-ta resistance gene-mediated defence response for producing transgenic plants resistant to fungal pathogens, especially rice blast fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2690 CAGCAGCCTACAGATCTGTAGCCAGCTGCAGCACCGCACTCTAAGACGTAATGTGTG--TA 2747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4435 CAGCGGACTATATTTTGTAGCCAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATA 4494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2748 TGACAGGTAGGACCAAGTATTAATAGTATAGTAAGCAACTATTGTATGAATTGGCTATTT 2807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a disease resistance protein of rice variety Tsuyuake. The rice Pi-ta gene was cloned by a map-based cloning strategy. The Pi-ta protein has a novel structure, compared to all known classes of resistance gene products. The Polynucleotide sequence confers a Pi-ta resistance gene-mediated defence response against diseases caused by fungal pathogens, particularly the rice blast fungus. Introduction of the cloned Pi-ta gene into susceptible rice confers resistance to pathogen strains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.7%; Score 137.4; DB 21; Length 5113; 85.5%; Pred. No. 3.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5113 BP; 1500 A; 1033 C; 1075 G; 1505 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 60-62; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                 (DUPO ) DU PONT DE NEMOURS & CO E
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/*tag= b
/number= 1
1592..3056
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3057..4898
/*tag= d
/number= 2
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                                                                                                                                                                                                                                                                                                                                                                                                         Valent BS, Bryan GT;
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Matches 165; Conserva
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                                                                                                                                                                                 WO200008162-A1
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21-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4457 CAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATATGACAAGTAGGACCAGGTATTA 4516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3319 CAGCTGCAGGACTCTAAGACGTAATGTGTG--TATGACAGGTAGGACCAAGTATTA 3376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a disease resistance protein of rice variety Yashiro-mochi. The rice Pi-ta gene was cloned by a map-based cloning strategy. The Pi-ta protein has a novel structure, compared to all known classes of resistance gene products. The polynucleotide sequence confers a Pi-ta resistance gene-mediated defence response against diseases caused by fingal parthogens, parthcularly the rice blast fungus. Introduction of the cloned Pi-ta gene into susceptible rice confers resistance to pathogen strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
            Disease resistance protein; rice; variety Yashiro-mochi; Pi-ta gene; resistance gene; Pi-ta resistance gene-mediated defence response; fungal pathogen; rice blast fungus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 2.4%; Score 121.8; DB 21; Length 5757; Similarity 86.0%; Pred. No. 7.5e-16; Conservative 0; Mismatches 22; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4517 AGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTACATTAACTATGAT 4567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5757 BP; 1638 A; 1202 C; 1251 G; 1666 T; 0 other;
                                                                                                                                                               /rote= "contains 1 intron"
1256..2200
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                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                             99WO-US17706.
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P-PSDB; AAY69307.
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                                                                           Oryza sativa.
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encoded protein, and mapping functional regions of protein
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                                                                                                                                                                                                                                              transgenic; stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its
1421 CGCAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAG-----GAGGGCGTTAG 1474
                                                        1475 CGAAGGACATCCCGGGACCGACGCCGCAGGTGCGTTGGAGTCGATGCCGTTGTGGAGCG 1534
                                                                    2620 CGAACGCCATTCCTGGACCTACTCCACACACTTTACCTGTGTCAATGTCAACGTGTAGTG 2561
                                                                                        GCTCGTGGGCCTCCTCCTCCTTCGGAGCTGCGGGGAGGCGGAGGATGGAGGGTTGGGGG 1594
                                                                                                 Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrice JL, Raines TM, Yu Y;
Ledford BL, Woessner JP, Haas I
Davis KR, Allen K, Hoffman N;
                                   2680 GGCACGGCACCAACCCGATCAGCTTTCCAGGCGATTCTTCACGGTTAG
                                                                                                                                                                                                                                             Arabidopsis thaliana, plant; insecticide; fungicide; transgenic
disease; crop; thale cress; tolerance factor; insect; pathogen;
                                                                                                                                                                                                                              Arabidopsis thaliana expressed polynucleotide SEQ ID NO 342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Price JL,
                                                                                                                                 2500 CGCAFTCCGGTGGAAGGATTTTATCCCA 2473
                                                                                                                       1595 GGCACTCGGGGGGAACCATGCGGTCCCA 1622
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Page A, Mathew AV,
Kricker M, Slater T,
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PAGE A.
MATHEW A V.
LEDFORD B L.
WOESSNER J P.
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HAMILTON C M.
                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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RAINES T M.
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GARCIA C A.
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ALLEN K.
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Rameaka JG,
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Hurban P;
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The invention relates to an Arabidopsis thaliana nucleic acid (I)

Comprising a sequence capable of hybridising under stringent conditions
to a sequence schecked from any one of 999 sequences (ARM93231),
Given in the specification or its fragment. A polypeptide (II) encoded by
Given in the specification or its fragment. A polypeptide (II) encoded by
Given in the specification or its fragment. A polypeptide (II) encoded by
Given in the specification or its fragment. A polypeptide (II) is
genetically modified cell (IV) comprising an exogenous nucleic acid or a
genetically modified cell (IV) comprising an exogenous nucleic acid, is
useful for screening a candidate agent for its biological effect. (I) is
useful in identifying homologous or related genes, in producing
compositions that modulate the expression or function of its encoded
protein, mapping functional regions of the protein and in studying
compositions that modulate the expression or function
associated physiological pathways. (I) is also useful in studying
composition of cells, particularly plant cells. (I) is also useful in
screening assays of various plant strains to determine the strains that
care best capable of withstanding a particular disease or environmental
stress. (II) and (III) are useful in improved methods of treating
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or treat disease. (II) are also useful in screening
crops to prevent or inhibiting production of a biosynthetic product in a
plant. (III) is useful in for identifying other mediators that may indect the biological innotion of the genetic function and regulation,
colerance to environmental stress, for ide
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Claim 1; SEQ ID NO 342; 49pp + Sequence Listing; English.
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 Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.
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     1597 CACTCCGGGGGAACCATGCCGTCCCA 1622
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                          1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCCTGGAGCGCGGGGACG 1362
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99US-0126264
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06-APR-1999;
16-APR-1999;
119-APR-1999;
21-APR-1999;
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14-JUN-1999;
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27-MAY-1999;
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                                                                                                                                                                                                                                Score 118.4; DB 21; Length 3108;
Pred. No. 3.1e-15;
0; Mismatches 191; Indels 6;
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990S-0161405.
990S-0161359.
990S-0161350.
990S-0161360.
990S-0161360.
990S-0161920.
990S-0161992.
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Best Local Similarity 55.8%;
Matches 249; Conservative (
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28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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PR 19-UTL-1999; 99US-0144311

PR 19-UTL-1999; 99US-0144312

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PR 20-UTL-1999; 99US-0144332

PR 20-UTL-1999; 99US-0144332

PR 20-UTL-1999; 99US-0144332

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Pred. No. 3.1e-15;
0; Mismatches 191; Indels 6;
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9905-0158029
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AAC41895 standard; DNA; 1024 BP

RESULT 11
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990S-0137528.
990S-0137502.
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99US-0138540.
99US-0138847.
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990S-0139452.
990S-0139453.
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99US-0139461.
99US-0139462.
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99US-0139459.
                                                                                                                                                25-FEB-2000; 2000EP-0301439
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                 17-OCT-2000 (first entry)
                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
                                                                                                                                                               25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
28-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
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24 - MAY - 1999)

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27 - MAY - 1999)

28 - MAY - 1999)

01 - JUN - 1999)

04 - JUN - 1999)

07 - JUN - 1999)
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18-70N-1999)
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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14-MAY-1999;
14-MAY-1999;
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10-JUN-1999;
10-JUN-1999;
                                                                                                           EP1033405-A2
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16-JUN-1999;
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30-APR-1999;
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AAC41895;
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and protein sequences isolated from encalyptus (Eucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth, environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
                                                                      1477 AAGGACATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGCGGC 1536
                                                                                                                                           1537 TCGTGGGCCTCCTCCTCCATCGGAGCTGCGGGAGAGGCGGAGGGGATGGAGGGGTTGGGGGCG 1596
1423 CAGGGGAÇGAGGCCGATGACAGGGAA-----CTGGCCGGAGCGAAGGAGGGCGTTAGCG 1476
                                  468 CACGGCACCAACCCGATCACAGCCGAATCTGTTTCCACGCGATTCTTCACCGCGTTAGCG 409
                                                                                                                                                                  Pinus radiata cell signalling involved polynucleotide SEQ ID NO:374.
                                                                                                 408 AAGGCCATTCCTGGACCTACTCCACACACTTTACCTGTGTCAATGTCAACGTGTAGTGGC
                                                                                                                                                                                                                 1597 CACTCCGGGGGAACCATGCCGTCCCAG 1623
                                                                                                                                                                                                                                                      288 CALICCGGIGGGAGGATITIAICCCAG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 176; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                                            AAA79573 standard; cDNA; 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-2000; 2000WO-US00724.
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99US-0162866.
                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pinus radiata.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                  AAA79573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1363 AGATCGGAGTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGCTCTCGAGGGCCGACCCTGGAGCGGCGGACG 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 528 ATCCTCTCGTACAAGTGGCTTCCACGCTCCCACTCTTTATCGCCGTTCCACGGGAAGCG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        708 ACCIGAAIAAIGGGAAGAAGAAGGIIGAAGAICAIGACGGAGGIICTIAAICAAACGA 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 recararrerecegracererecedicarecarerecarecerererea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     588 TACCACACACCCCCTTGATCTCTCCCCCCATTTCCTACTCTCCTCCGCTTCTTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Pred. No. 2.7e-15;
0; Mismatches 192;
                                                                                                                                                                                              9905-0154039.
9905-0155486.
9905-0155486.
9905-0155486.
9905-0156458
9905-0156458
9905-0157753
9905-0157865.
9905-0157865.
9905-0157865.
9905-0159293.
9905-0159293.
9905-0159294.
9905-0159294.
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990S-0160814.
990S-0160815.
990S-0160980.
990S-0160981.
990S-0161404.
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99US-0162142
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Matches 249; Conservative
                                                                                                                                                              99US-03
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13-OCT-1999;
13-OCT-1999;
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14-0CT-1999;
14-0CT-1999;
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18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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05-0CT-1999;
06-0CT-1999;
07-0CT-1999;
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22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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26-OCT-1999;
26-OCT-1999;
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7-SEP-1999;
                                                                                                                                                            13-SEP-1999;
15-SEP-1999;
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25-OCT-1999;
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12-OCT-1999;
                                                                                                                                               10-SEP-1999
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28-SEP-1999
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DB 20; Length 2380;

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The invention relates to an isolated hypoxia inducible promoter (HIP) obtained from the pyruvate decarboxylase (PDC) gene in rice. The HIP can be used for regulating the expression of foreign genes in cells such that the genes are expressed upon exposure of the cells to anaerobic conditions. The HIP can be used to produce transgenic plants that are more tolerant of anaerobic conditions, e.g. flooding. The HIP can also be used to enhance the expression of gene products that are normally induced under hypoxia conditions. The promoter can be operably linked to genes that express a protein product that is effective against solid tumours sequence obtained from rice pdc2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                         4381 GCTATAAACCAGCTATAAACATATTTTAAAGAGATAAAAGAAGAGGAGAATAGCAGCGG 4440
                                                                                                                                                                                                                                                                                                                                                                                                                                    4441 ACTATATATTTGTAGCCAGCTACAGCACGCACTCAAAGACGTAATGTGTGTATATGACAA 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAGGACCAGGTATTAAGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTACATTAA 4560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated hypoxia inducible promoter (HIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypoxia inducible promoter; HIP; pyruvate decarboxylase;
gene expression; transgenic plant; anti-tumour agent; ss.
                                                                                                                                                                                                                                                                                          Sequence 2380 BP; 759 A; 533 C; 425 G; 663 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice pyruvate decarboxylase (pdc2) gene sequence
                                                                                                                                                                                                                                                                                                                             Score 107.8; DB 2
Pred. No. 5.2e-13;
0; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated hypoxia inducible promoter
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                    Claim 2; Page 4-5; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВЪ.
                                                                                                                                                                                                                                                                                                                               2.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US18955
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                                                                                                                                                                                                                                                                                                                                                                     Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hodges TK, Huq E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY03900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1206 TTA 1204
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                                                                                                                                                                                                                                                                                                                               Query Match
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AAX31999/c
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                                                                              1;
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                                                                                                                                                                                                                                                                                                                                           1363 AGAICGGAGTAGAGGICGGIGCCCIIGGCCCAGICGGCCAICCIGGIGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                        1423 CAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGA------AGGAGGGCGTTA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1474 GCGAAGGACATCCCGGGACCGACGCCGCAGGTGCGTTGGAGTCGATGCCGTTGTGGAGC 1533
                                                                                                             1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGGCCCAGCGCACGGTGTCGCTTCTCCCCCTGG 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1534 GGCTCGTGGGCCTCCTCCCATCGGAGCTGCGGGGAGAGGCGGAGGATGGAGGGGTTGGGG 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCACTCCGGGGGAACCATGCCGTCCCAGTGGGACCCCACCACGCCCCCGCGCCCCGCGC 1653
                                                                                                                                                                                                                        486 TCGAGATTATGTTTATAGCTATTAGCATTCTTCTCAGATTCTGTATCACTTTCGCCTTGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 GCAAATATCATTCCAGGACCTACTCCACACTTTGTTATCTATATCGGCATGCAAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 ACCIGGAIGAAAAGGAGATCGGGAIGTTTCAGAICAGAGCGGATATCAIGGAIAAGICTC 487
                                                                                                                                                                                                                                                                                                      426 TACCAGAGAATTGCTCTTAGAACGCCTCCATGATTGAGAGCTGCCTTGGTTCTAGTTATC 367
                                                                                                                                                                                                                                                                                                                                                                                 366 ATATTCTTGTAGAGTGTGCTGTCCTTTTCCCATTCTTTGATCGCGGTACCTCCAATGGCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 CAGGGAACTAAACCAATACGAGCTTTTTTGGGATCTTTATAATGCTTCAGTATAGTGTTT 247
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 TIGCATICITGAGGAAGGAAATGATCCCAATGAGAACCATGAACTCCTCCCCTGCCCGAC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rice;
                                                                            9.
                                        Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice pyruvate decarboxylase (pdc2) gene promoter sequence
                                  Score 114.4; DB 21; Length
Pred. No. 1.1e-14;
0; Mismatches 236; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypoxia inducible promoter; HIP; pyruvate decarboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression; transgenic plant; anti-tumour agent; ss
Sequence 547 BP; 172 A; 116 C; 117 G; 142 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1654 AIGITCGACTGCCCTCCCAGGATGAACACCACCTTGTTCG 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated hypoxia inducible promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000/c
AAX32000 standard; DNA; 2380
                                      2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97us-0058639.
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                                                                            Conservative
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                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodges TK, Hug E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9913067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1998;
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                                                                        275;
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1594 186

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AAX32000;

PDC; rice;

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be used for regulating the expression of foreign genes in rice. The HIP can be used for regulating the expression of foreign genes in cells such that the genes are expressed upon exposure of the cells to anaerobic conditions. The HIP can be used to produce transgenic plants that are more tolerant of anaerobic conditions, e.g. ifooding. The HIP can also be used to enhance the expression of gene products that are normally induced under hypoxia conditions. The promoter can be operably linked to genes that express a protein product that is effective against solid tumours pdc2 gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                          4501 GIAGGACCAGGIATTAAGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTACATTAA 4560
                                                                                                                                                                                                                                                                  4441 ACTATATATTGTAGCCAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATATGACAA 4500
                                                                                                                                                                                                                                                                                                                                                                                                          New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice, chromosome 11; Indica rice cultivar; CO39; avirulence gene; AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding; resistance; agricultural; horticultural; plant protectant; ds.
                                                                                                                                                                                                    Score 107.8; DB 20; Length 5526; Pred. No. 7.3e-13;
                                                                                                                                                                                                                                     3;
                                                                                                                                                                        Sequence 5526 BP; 1438 A; 1322 C; 1289 G; 1477 T; 0 other;
                                                                                                                                                                                                                                     37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Durfee TJ;
                                                                                                                                                                                          2.2%; Scor.
78.1%; Pred. No. /...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 52-59; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chauhan RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD38801 standard; DNA; 15686 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USDA ) US DEPT OF AGRICULTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice RGA38 contig.26Nippon DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000; 2000US-242313P.
09-JUL-2001; 2001US-303897P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-OCT-2001; 2001WO-US46331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                      Best Local Similarity 78.1 Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leong SA, Farman ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-471442/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200234927-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4561 CTA 4563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD38801;
                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene ANRI-CO39. The Pi-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-CO39(t) nucleic acids may be used as probes to detect the presence of and/or expression of Pi-CO39(t) genes, and to produce large quantities of pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(t).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2,
                                                                                                                                                                                                                                                                                                                                                       as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4181 CAACGTTTGACCATTCGTCTTATTTGAAAAAGATTATGATTAGTATTTTTATTGTTATT 4240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9054 CCAACTTTGATCGTCGTTTTTATTTGAGAAATTTTTATAATTAGTATTTTTTGTTATG 9113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTTTTCAAATAAGACGGATGGTCAAAGCGCTAAACATGGATATCTATGGCTACACTTA 4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9172 AAATTTTCAAATAAGACAGACGATTAAA--GTTGGGCGCGGAAAACTATGGTTACACTTA 9229
                                                                                                                                                                                                                                                             polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or horticultural applications. The present directly is rice RGA38 contig.26Nippon DNA. This sequence comprises portion of BAC clone 82NO3 from Nipponbare, containing RGA38 sequence well as ores NBR5 and NBR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 99; DB 24; Length 15686; Pred. No. 8.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15686 BP; 4645 A; 3184 C; 3204 G; 4653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 150; Conservative
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OM nucleic

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BQ237748 TABD5012F

AQ573895 IDXXD0041B

AQ589925 IDXXD0034K

BG560351 RH1Z2_73_BE213308 ESTF0065 T

AQ280077 IDXXD0032K

AQ280071 IDXXD0032K

AQ274081 IDXXD0032K

AQ364616 IDXXD0032K

AQ364616 IDXXD00782

BG102400 RH1Z2_23_AQ689068 IDXXD00782

BG102400 RH1Z2_23_AQ689068 IDXXD00782

AQ364610 IDXXD00780

AQ364510 IDXXD0070K

AQ4510 IDXXD0070K

AQ5794105 IDXXD0070K

AQ5794105 IDXXD0079E

AQ156838 IDXXD0079B

AQ156838 IDXXD0079B

AQ564314 IDXXD0079B

AQ64414 IDXXD0079B

AQ64414 IDXXD0079B

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BF619879 HVSMEC000
AQ576807 nbxb0089H
AU097543 AU097543
B1956651 HVSMEn000
BH643146 1008052E0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryoriy Viridiplaniae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU065751 Rice cDNA from immature leaf including apical meristem Orvza sativa (japonica cultivar-group) cDNA clone E51292_1A, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsukuba, Ibaraki

    465
/organism="Oryza sativa (japonica cultivar-group)"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki, F. and Yamamoto, K.
Rice cDNA from immature leaf including apical meristem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2, 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                        AQ689068
BF473797
AQ869102
AZ135604
AQ446510
AQ446510
                                                                                                                                                                                                                                                                                                                                                                                                      AC 794105
ALB 29579
AQ 156838
AZ 047724
AQ 689393
BQ 253395
AQ 864314
AQ 914146
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AQ868460
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AU065751
AU065751.1 GI:4968847
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROJECT = 'RGP'
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AU065751/c
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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     AU065751 AU065751
AU030601 AU030601
BE490225 WHE0366 H
D4752 RICS13122A
BO240809 TaED5012F
AZ918792 1006008A0
                                                                                                                   March 25, 2003, 19:50:00 ; Search time 5095.83 Seconds
(without alignments)
15894.084 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                        1 aggggacactacactttcca......tgccgccggagtgcgccccg 5001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                          32308132
                     GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                       US-09-702-134-7212_COPY_62300_67300
                                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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AU030601
BE490225
D47552
BQ240809
AZ918792
                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 1.0
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em_gss_vrt:*
em_gss_fun:*
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Maximum DB seq length: 2000000000
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gb_est5:*
em_estfun:*
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Total number

Database

Result No.

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Searched:

Sequence:

EST 02-APR-2002

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BE490225
BE490225.1 GI:9609758
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                                                                                                                                                                                                             Matches 341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bread wheat.
                                                                                                                                                                                               Similarity
                                                                                                                                       128
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Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 498)
Sasakl, T. and Yamamoto, K.
Rice CDNA from immature leaf including apical meristem
                                          /clone_lib="Rice cDNA from immature leaf including apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU030601.
AU030601 Rice cDNA from immature leaf including apical meristem Oryza sativa (japonica cultivar-group) cDNA clone E51292_22, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                       1426 GGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGACATC 1485
                                                                                                                                                                                                                                                                                   1486 CCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGCGGCTCGTGGGCC 1545
                                                                                                                                                                                                                                                                                                                                             1546 TCCTCCCATCGGAGCTGCGGGAGAGGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGG 1605
                                                                                                                                                                                                                                                                                                                                                                                                     1606 GGAACCATGCCGTCCCAGTGGGACCCCACCACGCCCCGCGCCCCGCCATGTTCGACTGC 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                      274 TCCTCCCATCGGAGCTGCGGGAGAGGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                         /note="Organ: leaf; immature leaf including apical
                                                                                                                                                                                              ;;
                                                                                                                                                              Score 375.8; DB 9; Length 465; Pred. No. 1e-57; 6; Mismatches 5; Indels 1
                                                                                                    meristem (under long day condition)"
1 160 c 138 g 90 t 5 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1786 GGCCTGGGGGTTGGGTTTGGGACAATAATTTG 1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                         /dev_stage="immature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                            /clone="E51292_1A"
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AU030601.1 GI:3763862
                                                                                                                                                              7.5%;
98.5%;
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                             meristem"
                                                                                                                                                                                            Matches 388; Conservative
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POLYA=No.
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                                                                                                                    72
                                                                                                                                                                Query Match
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Triticum aestivum
Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida: Poales; Poaceae; Pooideae;
'Triticeae; Triticum.

1 (bases 1 to 555)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han Anderson,O.D., Chao,S., Choi,D.W., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE490225 555 bp mRNA linear EST 31-JUL-2000 WHE0366_H01_P02ZS Wheat cold-stressed seedling cDNA library Triticum aestivum cDNA clone WHE0366_H01_P02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Oll Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Wipponbare"
/db_xxref="krann:39947"
/clone="E51232.2z"
/clone="E51222.zz"
/clone="E51222.zz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 GAAAAGTAGAACATAAGGTGCGTAGTCTCTTAGCTATTTATCTGATAAAAGAAAAACAAC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 ACAGAGAGGACTAGAGCGTGGAAGTACCATAGTTCAAATAGGCTTGAGCCAACATATGTC 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 ACAGAGAGACTAGAGCGTGGAAGTACCATAGTTCAAATAGGCTTGAGCCAACATAGTC 277
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
                                                                                                                                                        meristem"
//dev_stage="immature"
//dev_stage="immature"
//note="organ: leaf; immature leaf including apical
meristem (under long day condition)"
a 125 c 118 g 127 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTATATTGCCCAAGCCCTGATGCTAGTCCTACCTGAAACACCAAACAGAG 449
                                                                                                                                                                                                                                                                                                                                                                                    Length 498;
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                                                                                                                                                                                                                                                                                                                                                                                Score 334.4; DB 9;
Pred. No. 2.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.
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TaE05012F06R TaE05 Triticum aestivum cDNA clone TaE05012F06E, MRNA
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                                                                                                                           Contact: Takuji Sasaki
Mational Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Isukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4861
                                                                                                                                                                                                                  Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4862 TGCTCGCCACCACGCCCACGCCCACGCCGACGCCGACGCTGATATTCCTTTTGG 4921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 GOGGGGAGTCCAACATGGGCGGTCNCGC-GNGGCACCAACGGNCCGTGGGAACCCGTGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
/note="Green shoot (8 days old)"
/note="Green shoot (9 days old)"
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe RG, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 254.6; DB 14; Length 309;
Pred. No. 8e-36;
0; Mismatches 16; Indels 3;
         Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 309)

Sasaki,T., Miyao,A. and Yamamoto,K.

Rice cDNA from callus 1995

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Matches 293; Conservative
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                                                                                                                                                                                                                                                                                            PROJECT = 'RGP'
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                                                        AUTHORS
TITLE
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/organism="Triticum aestivum"

(dultyar="Chinese Spring"

(dultyar="Chinese Spring"

(dollar="Chinese Spring"

(clone="WHE0366_H01_P02"

(clone="WhE0366_H01_P02"

(dev_stage="Five-day old seedling"

(dev_stage="Vector: Lambda Uni-ZAP XR, excised phagemid;

Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized

(site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized

(site_1: more and grown aseptically in the dark at room

temperature on filter paper with water, nystatin and

cefotaxime in covered crystallization dishes. Five-day

old seedlings were transferred to 5 C cold room and kept

for a cold seedlings were transferred to 5 C cold room and kept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 bp mRNA linear EST 03-APR-2002 CDNA, mRNA sequence.
D47552 B47552.1 G1:701261
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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                    for 48 hr. The tissue, total RNA, and poly(A) FNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1243 GCCATCCGGCGGCGTACICGTTGGCGTCGCCCAGCGCACGGTGTCGCTCTCCCCCTGG 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1363 AGAICGGAGIAGAGGICGGIGCCCIIGGCCCAGICGGCCATCCIGGIGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1423 CAGGGGACGAGGCCGATGACAG-----GGAACTGGCCGGAGCGAAGGAGGGCGTTAGCG 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1477 AAGGACATCCCGGGACCGACGCCGCAGGTGCGGTTGCAGTCGATGCCGTTGTGCAGCGGC 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1537 ICGIGGCCICCICCATCGGAGCTGCGGGGAGAGGCGGAGGATGGAGGGGTTGGGGGGCG 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1303 TACCAGAGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCCTGGAGCGGCGGACG 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ATGTCCGGGTACAGCTCCGACCCCTTGCCCCACTCGGCCATGCCCCGGACGGCG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 CCCATGCGGCGCGCGCGTACTCGCTGGCGTCGGCCCAGCGCTGTCGCTCTCGCCCTGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 274.2; DB 1
80.0%; Pred. No. 2.1e-39;
tive 0; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other authors).
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/note="Organ: Jeaf; Vector: RescueMu (engineered from PBlueScript backbone); Site_1: BamHI; Site_2: BgllI; RescueMu is a 4.9 kb, modified maize Mu transposon RescueMu is a 4.9 kb, modified maize Mu transposon RescueMu is a 4.9 kb, modified maize Mu transposon. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'RescueMu,' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digseted using BanHI and BgllI, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 22-OCT-2001
                                                                                                                                                                  Sequence was trimmed at very probable ligation site. Post-ligation sequence submitted separately.

Plate: 1006008 row: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGATGACAGGGAAC-----TGGCCGGAGCGAAGGAGGCGTTAGCGAAGGACATCCCG 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1546 TCCTCCCATCGGAGCTGCGGGGAGAGGCGGAGGATGGAGGGGTTGGGGGGCGCACTCCGGG 1605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 GGCCCACCCCGACGCGTGGTTGGCGGCGTGCATGCCGGCGTGCAGCGGCTCCCGCGCC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 GCACCGATGCGGCCCCCCGTCTCGACGCGACCCTGGCCGGGCGCACTCTCGGCGTAG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 AGCTCGGTGCCCCTGCCCCACTCTGCCATCCGCGTGCCTCCCCAGGGGACGAGGGACGAGG
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                                                                                                                                                                                                                                                                                                                                                         background W23/A188/B73"
                                                                      855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fex: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1666 CCICCCAGGAIGAACACCACCIIGIICGACGGAGGGAGG 1704
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                          Department of Biological Sciences
                                                                                                                                                                                                                                                                                                    1. .486
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="leaf"
                                                                                                                                                                                                                                                Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                 /cultivar="mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ampicillin.
                                                    Stanford University
     Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
BF619879/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                              /tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="8. coli DH108"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
NotI: Site_2: MluI; mRNR obtained from wheat seeds of
cultivar Glenle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
~i
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                    Email: scloutier@em.agr.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >2.0 kb Plate: 012 row: F column: 06 Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1506 GCGGTTGGAGTCGATGCCGTTGTGGAGCGGCTCGTGGGCCTCCTCCCCATCGGAGCTGCGG 1565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1452 -----GCCGGAGCGAAGGAGGCCGTTAGCGAAGGACATCCCGGGACCGACGCCGCAGGT 1505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1332 GGTCTCGAGGGCGACCCTGGAGCGGCGGACGAGATCGGAGTAGAGGTCGGTGCCCTTGGC 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1392 CCAGTCGGCCATCCTGGTGCCGCCGACGCGCAGGGGACGAGGCCGATGACAGGGAACTG 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 GGTCTCCACGGCGGCGCGCGCGCACCATGTCGTACAGCTCCGACCCCTTGCC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 CGCGCCCCGGAGCGAGCACGAGCGTTGGCGAAGGACATCCCGGGGCCGACCCCGCAGGT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 GGCCCAGCGCACGGTGTCGCTCTCGCCCTGGTACCACACCACGCCCCCGATCCGGCCGCC 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ918792 486 bp DNA linear GSS 177
1005008A02.yl 1006 - RescueMu Grid G Zea mays genomic, DNA
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6%; Score 230.4; DB 14; Length 78.1%; Pred. No. 1.8e-31; Live 0; Mismatches 76; Indels
                                                                                                                                                                                                 1. .381
/organism="Triticum aestivum"
/cultivar="Glenlea"
                                                                                                                                                                                                                                                                        /db_xref="taxon:4565"
/clone="TaE05012F06R"
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       /clone_lib="TaE05"
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Walbot, V.
Fax: (204) 983-4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 78.1 Matches 292; Conservative
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AQ576807

174 bp DNA linear GSS 02-JUN-1999
nbxb0089H04r CUGI Rice BAC Library Oryza sativa genomic clone
nbxb0089H04r, DNA sequence.
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1 (bases 1 to 774)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGGCCCAGCGCACGGTGTCGCTCTCCCCCTGG 1302
                                                                                                                               1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCCTGGAGCGGCGGCGACG 1362
                                                                                                                                                                                                                                                                  1363 AGAICGGAGIAGAGGICGGIGCCCTIGGCCCAGICGGCCAICCTGGIGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                                                                                  1423 CAGGGGACGAG-----GCCGATGACAGGGAACTGGCCGGAGCGAAGGAGGGCGTTA 1473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515 TCCACGTTCCCCTGGTATGCCGCCGTTTCGGCATCGGACTATGCATCGCTCTCCCCTGG 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="nbxb0089H04r"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
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Location/Qualifiers
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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/db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /nace-Wector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, polyfich RNA was purfied, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(·) cDNA phagemids. These steps were performed in the fu Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University of California, Riverside (Choi, Close, Fenton). Phagemids were performed at CUGI (Ming, Tu, Frisch, Henry, Simmons, Oates Performed at CUGI (Ming, Tu, Frisch, Henry, Simmons, Oates Kambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see hittp://www.genome.clemson.edu/projects/parley. To order this clone see http://www.genome.clemson.edu/projects/parley. To order this clone see http://www.genome.clemson.edu/projects/parley also see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genemics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.lada.gov/gepages/bgn/31/cover.html)" 91 a 198 c 203 g 96 t
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/lab_host="TJC121"
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/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Total hg bases = 342
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 583.
Location/Qualifiers
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   IVSMEc0009122f, mRNA sequence.
                                                               BF619879.2 GI:13107874
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Bordeum vulgare.

Hordeum vulgare.

Hordeum vulgare

Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

(Dases I to B16)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,

Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons

J., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 22-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                         98 IITAATTATACCAAGCCAATTCAATAATCATAAGAATGAGTGGTCCATGAAACTAAATAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 ACAGNGNGGNCTAGAGCGNGGAAGTNCCNTAGTTCAAAAAGGNTTGNGCCAACANATGCC 45
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                 /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                     Length 273;
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 CAAGCTGGACTTGCCCTTGGGTGCTAAGGTGCAGATGGCCATCT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 187.4; DB 9;
Pred. No. 1.1e-23;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total hg bases = 236
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 372.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEn0004J09f"
                                                                    /cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Rachis"
/lab_host="TJC121"
Location/Qualifiers
1. .273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI956651.1 GI:16307904
                                                                                                                                                                                                                                                                                     3.7%;
                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.3
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .816
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BI956651/c
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SOURCE
    FEATURES
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                                                                                                            and subtropies, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mpp (Arumuganathan haploid genome equivalent of 431 Mpp (Arumuganathan haploid genome equivalent of 431 Mpp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety The of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU097543 Linear EST 03-APR-2002 AU097543 Rice shoot Oryza sativa (japonica cultivar-group) cDNA close 85064, mRNA sequence.
AU097543 AU097543.1 GI:8860225
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Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magrollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                         HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4281 ITITITIAATATTTTTTTAATTTTTTCAATAAGACGGATGGTCAAGCGCTAAACATG 4340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4161 GITTIPAGCACTATICATGTTCAACGTTTGACCATTCGTCTTATTTGAAAAAGATTATGA 4220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4221 TTAGTATTTTTATTAGTGATGATAAAACATGAATAGTACTTTATGTGTGACTAATT 4280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 TIAGTATTTTTATTGTTATTATATGATAAACATAAATAGTACTTTATTTGTGACTAA-- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 CCAAAAAAAGCCGTCCTACGCAGTTTTACGTGCTACTACTACCTCCCAAAATAAGTGTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                        /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 188.4; DB 1
Pred. No. 5.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki,T. and Yamamoto,K.
Rice cDNA from etiolated shoot (2000)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%;
Similarity 82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 273)
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Best Local Si
Matches 228;
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AU097543/c
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SOURCE
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pBlueScript backbone); Site_1: BamII: Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.lastate.edu and follow the links for
RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE443619 613 bp mRNA linear EST 25-JUL-2000 WHEIL16_B08_D16ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHEIL16_B08_D16, mRNA
                                                                                                                                  Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008052 row: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1371 GTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCTGCCGCCGACGGCGCAGGGGAC 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1542 GGCCTCCTCCCATCGGAGCTGCGGGAGAGGCGGAGGATGGAGGGGTTGGGGGGCGCACTC 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGCCGATGACAGGGAAC-----TGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGACAT 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1485 CCCGGGACCGACGCCCCAGGTGCGGTT---GGAGTCGATGCCGTTGTGGAGCGGCTCGTG 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1602 CGGGGGAACCATGCCGTCCCAGTGGGACCCCACCACGCCCCCGGGCCCCGCCATGTTCGA 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 GTAGAGCTCGGTGCCCCTGCCCCACTCTGCCATCCGCGTGCCTCCCACGCGCGCAGGGGAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 CCCGGGGCCCACCCCGACGGCGTGGTTGGTTGATGCCGGCGTGCAGCGGCTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 GAGCCCTACCACGCCCCCCCCCCGCGGCCCCGAGCACCGCGTTGGCGAACGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17; Length 394;
                                                                                                                                                                                                                                                                                                                                       /cultivar="mixed background W23/A188/B73"
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                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="1008" RescueMu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
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                                    Stanford University
SS California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%; Score 178.6; DB 17; ilarity 74.3%; Pred. No. 3.9e-22; Conservative 0; Mismatches 79;
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               Biological Sciences
                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
                                                                                                                                                                                                                                    Class: transposon-tagged.
Location/Qualifiers
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Matches 255;
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BE443619/c
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ORIGIN
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KEYWORDS
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Anote="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Moli, plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachiese were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified colm library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis were serformed at CGI sequence analysis are setting and sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  this clone see http://www.gencme.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/pgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1384 CCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGCGCAGGGGACGAGGCCGATGACA 1443
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1008052E03.y1 1008 - Rescuemu Grid I Zea mays genomic, DNA
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Pred. No. 1.9e-22;
0; Mismatches 85; Indels
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Walbot, V.
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/note="Vector: pSPORT-P" (Invitrogen Technologies); Site_1: NotI; Site_2: Mlu1; mRRA obtained from wheat seeds of cultivar Glenlea 5 days post-anthesis" 100 c 107 g 107 t
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(bases 1 to 446)
                                                                                                                                                                                                                                                                                                                                                                                               BQ237748 1inear EST 03-MAX-2002 TAE05012F06F TAE05 Triticum aestivum cDNA clone TaE05012F06F, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheat functional genomics - Glenlea developing seeds cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >2.0 kb Plate: 012 row: F column: 06 Seq primer: M13 Forward.
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   336 AGCATATGTCCCAGCTGGACCTGAGCCTGGGTGTTAAGATGCAGATGCCGTCTTGGAAC 277
                                                              328 GGCAAACCCTTTGCATCAACAAATCTCACGTTTCGAAGTTTGATCCCTTTCTGAGCTTCC 387
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                                                                                          276 GGCAACCCCATCGCATCGACAACCTCACGTTCCGAAGTTTTAAGCCCTTCTGAGCTTCC
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Conteact: Dr. Sylvie Cloutier
Coreal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
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                                                                                                                                                                                                                   216 CITACGACTICGGTGTACTGCCCAAGCCCTGATGCCAGCCCAACCTGGA 168
                                                                                                                                                                                    388 CITACTACTTCAGTATATTGCCCAAGCCCTGATGCTAGTCCTACCTGAA 436
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/dev_stage="5 days after anthesis"
/lab_host="E. coli DH10B"
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Pred. No. 4.7e-20;
0; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
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Local Similarity 66.7%;
Les 273; Conservative
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//dev_stage="Fige and circleted seedling"
//dev_stage="Fige and circleted seedling"
//def_stage="Fige and circleted seedling"
//def_stage="Fige and circleted seedling seed phagemid
pBluescript SK; Site_1 EcoRI; Site_2: KhoI; Seeds were
surface-sterilized germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxine in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Ghoi, Close, Fenton) at the University of
California, Riverside. The CDNA clones were in vivo
                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae; Triticum.

(bases 1 to 613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California, Riverside. The CDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Universisty. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Wheat etiolated seedling root normalized cDNA
                                                                                                                                               Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 CATTGGCATAT----TTATACCAATCAAATTCATGAATTTTAAGAATGGTGGTGCCAGCG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
Location/Qualifiers
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="WHE1116_B08_D16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: oandersn@pw.usda.gov
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nbxb0041B05f CUGI Rice BAC Library Oryza sativa genomic clone
nbxb0041B05f, DNA sequence.
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1 (bases 1 to 842)
Wing.R.A. and Dean.R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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                                                                                                                                             4126 TAGAATAGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAACG 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4306 TICAAATAAGACGGATGGTCAAAGCGCTAAACATGGATATCTATGGCTACACTTATTTTG 4365
                                                                                                                                                                                                                                                                                       272 TATACTCCTACTCCCTCTGTCCCAAATAAGTGCAGTTTT-GCACTATTCACGTTCAAGG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 535;
                                                                                    Indels
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/clone="nbxb0041B05f"
/clone_lib="CUGI Rice BAC Library"
                              Score 164.8; DB 17;
Pred. No. 1.1e-19;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Octoan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/lab_host="E. coli DH10B"
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Class: BAC ends
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High quality sequence stop: 189.
Location/Qualiflers
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/cultivar="Nipponbare"
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                              3.3%;
                                                         Best Local Similarity 85.8 Matches 218; Conservative
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                                 Query Match
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AQ327645/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 bp DNA linear GSS 02-JUN-1999 nbxb0083A09r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0083A09r, DNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza
181 GCT-----ACCAGGAAAACTAGTGTTTGAATGTACCATAAGTCAAATAGGACTGAGCC 233
                                                         268 AACATATGTCCAAGCTGGACTTGCGCTTGGGTGCTAAGGTGCAGATGGCCATCTTCTAGT 327
                                                                                                            234 AGCATATGTCCCAACTGGACCTGAGCCTGGGTGTTAAAATGCAAATGGCCGTCTTGGAAC 293
                                                                                                                                                                                                   1 (bases 1 to 535)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (q1998)
                                                                                                                                                                        GGCAAACCCTTTGCATCAACAAATCTCACGTTTCGAAGTTTGATCCCTTTCTGAGCTTCC
                                                                                                                                                                                                                                                                                                                     388 CTTACTACTTCAGTATATTGCCCAAGCCCTGATGCTAGTCCTACCTGAA 436
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Clemson University
100 Oradan Hall, Clemson, SC 29634, USA
Tat: 864 656 7288
Fax: 864 656 4293
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Location/Qualifiers
1..535
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Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
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/clone="nbxb0083A09r"
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AQ573895.1 GI:4973696
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order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa. Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
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                                                                                                                                                                                                                                                                                                                                                                                                                   4312 TAAGACGGATGGTCAAAGCGCTAAACATGGATA--TCTATGGCTACACTTATTTTGGGAC 4369
Arabidopsis, makes it suitable for genomic studies. In
                                                                                                                                                                                                                                                                                                                                       4132 AGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAACGTTTGAC 4191
                                                                                                                                                                                                                                                                                                                                                              5; Gaps
                                                                                                                                                                                                                                                        Query Match 3.3%; Score 163.6; DB 17; Length 842; Best Local Similarity 88.0%; Pred. No. 1.7e-19; Matches 213; Conservative 0; Mismatches 24; Indels 5;
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Search completed: March 26, 2003, 07:53:11 Job time : 5117.5 secs

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TYPE: DNA
ORGANISM: Oryza sativa
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 US-09-575-574-5
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                                                               March 26, 2003, 04:38:30 ; Search time 123.698 Seconds (without alignments) 12398.686 Million cell updates/sec
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                                                                                                                            1 aggggacactacactttcca......tgccgccqqaqtgcqcccq 5001
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Sequence 6,
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/bervs_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/bervs_COMB.seq:*
       GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-575-574-3

US-09-575-574-2

US-09-130-114-2

US-09-105-390-13

US-09-105-390-13

US-09-105-390-14

US-09-105-390-5

US-09-105-390-5

US-09-103-840A-2

US-09-105-537-1

US-09-105-537-1

US-09-105-537-1

US-09-107-649-7

US-09-197-649-7

US-09-197-649-7

US-09-197-649-7

US-09-197-649-7

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US-07-704-288C-1
US-08-379-259-1
US-08-387-942C-1
US-08-258-261B-6
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US-09-103-840A-1
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5212296-8
                                                                                                                                                                             441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                             - nucleic search, using sw model
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1590 4 UK
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1.8 5572 4
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1.4 7218 1
1.2 4403765
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) Sequence 5, Application US/09575574
) Patent No. 6376750
) GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Chao, Yu-Chan
) TITLE OF INFORMION: PLANT SEEDLING AND EMBRYO PROMOTER
TITLE OF INFORMION: PLANT SEEDLING AND EMBRYO PROMOTER
CURRENT APPLICANTON NUMBER: US/09/575,574
) CURRENT FILING DATE: 2000-05-22
) NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
) SEQ ID NO 5
IENGTH: 1730
US-08-456-837-6
US-08-457-342-6
US-08-458-076A-6
US-08-458-076A-6
US-08-457-333A-4
US-08-457-333A-6
US-08-029-034-6
US-09-029-934-6
US-09-029-603-4
US-09-020-603-4
US-09-020-603-4
US-09-072-594-16
US-09-072-594-16
US-09-072-594-16
US-09-072-594-16
US-08-343-428-1
US-08-843-428-1
US-08-843-428-1
US-08-843-428-1
US-08-843-428-1
US-08-844-173-4
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US-09-575-574-3/c
; Sequence 3, Application US/09575574
; Patent No. 6376750
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
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RESULT 4
US-09-249-585A-4/c
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Pred. No. 3.6e-12;
0; Mismatches 79; Indels 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Yu, Su-May
APPLICANT: Chao, Yu-Chan
TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER
FILE REFERENCE: 08919-047001
CORRENT APPLICATION NUMBER: US/09/575,574
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 500
         TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER FILE REFERENCE: 08919-047001
CURRENT APPLICATION WUMBER: US/09/575,574
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 3572
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; Sequence 2, Application US/09575574
; Patent No. 6376750
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Matches 168; Conservative
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APPLICANT: Chao, Yu-Chan
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; ORGANISM: Oryza sativa
US-09-575-574-2
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US-09-575-574-3
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Best Local Similarity
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APPLICANT: HOTIGK, ROBERT
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
LENGTH: 1926
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APPLICANT: HOTLICK, RObert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
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| LOCATION: (1)..(1926)
| STHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4
Sequence 4, Application US/09249585A Patent No. 6417002
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US-00-130-114-2/c
Sequence 2, Application US/09130114
Patent No. 5976807
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ORGANISM: Epstein Barr Virus
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4375 TAGTAGGCTATAAACCAGCTATAAACATATTTTAAAGAGATAAAAGAAGAAGAGAGAATAG 4434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 73.2; DB 4; Length 1026; 75.3%; Pred. No. 5e-08; tive 0; Mismatches 33; Indels 6
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Sequence 5, Application US/09105390
Sequence 5, Application US/09105390
Patent No. 6288303
FRIEAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4490 GTATATGACAAGTAGGACCAGGTATTAAGAGTATAGTA 4527
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  SOFTWARE: FastSEQ for Windows Version 2.0 CORRENT APPLICATION DAPA. BAPLICATION NUMBER: US/09/105,390 FILING DATE: Filed herewith
                                                                 FILING DATE: Filed herewith
CLASSIFICATION
PRICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-UIN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REPERRENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: PELILINORY, JOANNE R.
RESISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Dehlinger & Associates 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60/050,675
                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 13.
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 75.3
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                      TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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TOPOLOGY:
US-09-105-390-13
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1931;
                                                                                                                                                                                                                                                           Score 74; DB 2; Length 193
Pred. No. 4.5e-08;
0; Mismatches 255; Indels
TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/LD903US1
CURRENT APPLICATION WOMBER: 08/09/130,114
CURRENT PILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-105-390-13

Sequence 13, Application US/09105390

Sequence 13, Application US/09105390

PATENT NO. 6288303

TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

TITLE OF INVENTION: and Genes

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA
                                                                                                                                                                                                                                                           1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER; IBM COM-
OPERATING SYSTEM:
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-09-130-114-2
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                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 CAGCGGGCTACAGATTTGTAACCACCTACAGCAAGACTTTAAGATGCATGTGTATAA 401
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Pred. No. 7.6e-08;
0; Mismatches 33; Indels 6
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APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8

US-08-232-463-14/C
US-08-232-14/C
US-08-23
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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IIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
COMPUTER: REA PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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TELECOMMUNICATION INFORMATION:
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5%;
                                                                                                                                    INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2169 base pairs TYPE: nucleic acid STRANDEDNESS: single
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(703)683-4109
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TYPE: nucleic acid
STRANDEDNESS: single
                              TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.5
Best Local Similarity 75.3
Matches 119; Conservative
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US-09-105-390-5
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STATE:
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DB 3928207 CGCCGGCCCCCGCCCCCGCCGGTGCCGCCGATCCCCCCGTCGCCGGGAACACCGGCGC 3928148
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                       1181 ATACCTGGATGAGGAGAAAGGTGTGGCATGGCGAGATCGGCGCCCAGGTTGCGGACGAGCA 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1382 TGCCCTTGGCCCCAGTCGGCCATCCTGGTGCCGCCGACGCGCAGGGGACGAGGCCGATGA 1441
                                                                                                                                                                                                                         1241 TGGCCATCCGGCGGGGGTACTCGTTGGCGTCGGCCCAGCGGTGTGGGTGTCGCTCTCCCCCT 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRANT APPLICANTION NUMBER: US/09/103,840A
CURRANT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                           Gaps
                                                                                                                                                                         0
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47.7%; Pred. No. 0.005;
                                                                                                                        DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 260; Indels
                                                                                                                                                                         Indels
                                                                                                                     Query Match 1.4%; Score 70.6; DB 1; I Best Local Similarity 5.9%; Pred. No. 6.3e-07; Matches 19; Conservative 194; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-103-840A-2/c; Sequence 2, Application US/09103840A; Patent No. 6284328; Elent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1301 GGTACCAGAGGACAGCGCCGA 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, OWEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 244; Conservative
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; TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-F1s
US-08-232-463-14
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Best Local Similarity
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SEQ ID NO 2
LENGTH: 4403765
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Sequence 4, Application US/09060756

Sequence 4, Application US/09060756

Setent No. 6183957

GENERAL INFORMATION:

APPLICANT: Cole, Stewart

APPLICANT: Buchrieser-Brosch, Roland

APPLICANT: Buchrieser-Brosch, Roland

APPLICANT: Buchrieser-Brosch, Roland

APPLICANT: BLilault, Alain

TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

FILE REFERENCE: 3495-0169

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

CORRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

CORRENT FILING DATE: 1998-04-16
     DD 1191405 AGCCGGC-CGACCCGCCGTCGCCACCGCGGCCGCCGCCGCCCCCCTCCGCCGCCGCACCG 1191463
                                                                                                    1191285 CGCCGCCTCCGCCGGTGCCGCCGTTGCCCGACAGCCGGCTGACCCGCCGTTGCCGC 1191344
                                                                                                                                                                                                   1191345 CGTTGCCGGCGTTGCCGCCGCCGCCGCCGTGCCGGCGTCGCCGTTGCCGGCACAGCC 1191404
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                                                    1517 CGAIGCCGTIGTGGAGCGGCTCGTGGGCCTCCTCCCATCGGAGCTGCGGGGAGAGCGGGA 1576
                                                                                                                                                      1577 GGATGGAGGGGTTGGGGGGCACTCCGGGGGAACCATGCCGTCCCAGTGGGACCCCACCA 1636
                                                                                                                                                                                                                                                      1637 CGCCCCCGCCCCCGCCATGTTCGACTGCCCTCCCAGGATGAACACCACCTTGTTCGACG 1696
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Pred. No. 6.2e-05;
0; Mismatches 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.2%;
Best Local Similarity 46.0%;
Matches 204; Conservative
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US-09-060-756-4
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Db 3928087 TGCCGCCGTCCCCGCCGATGCCGCCTTGGCCGCCGTCGGGGTCGGGTCGGCGATCA 3928028
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPRENDENCE: 24366-20007,00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
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ilarity 46.6%; Pred. No. 0.005;
Conservative 0; Mismatches 287; Indels 1;
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CTHER INFORMATION: H37Rv
US-09-103-840A-1
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
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US-09-103-840A-1
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Best Local
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CORRESPONDENCE ADDRESS:
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45.5%; Pred. No. 0.00026;
Live 0; Mismatches 259; Indels 0;
                                                                                                                                                           Sequence 1, Application US/09105537A
Patent No. 6265202
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, Y.
TITLE OF INTENTION: DNA encoding methymycin and pikromycin
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PSPLICANT: McGee, J. D.
TITLE OF INVENTION: Plant Pathogen Induced Proteins NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15872
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; Sequence 3, Application US/08728956
; Patent No. 5677175
                                             498 GGACACCGGTGGGGACGCCGGGG 520
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; ORGANISM: Streptomyces venezuelae
US-09-105-537-1
                1604 GGGGAACCATGCCGTCCCAGTGG
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Matches 216; Conserv
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US-09-105-537-1/c
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APPLICANT: Tuerk, Craig
APPLICANT: Fluor, David
APPLICANT: Smith, Jonathan D.
TIPLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXO2/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
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                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IEBA PC COMPALIBLE
COMPOTER: IEBA PC COMPALIBLE
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 7.8e-05;
                                                                                                                                                                                                                                                                         CLASSIFCATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Breen, John P.
REGISTATION NUMBER: 3220-26119
REFERENCE/DOCKET NUMBER: 3220-26119
TELECOMMUNICATION INFORMATION:
TELEFONE: (317)231-7745
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1591 base pairs
                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,956
E: Barnes & Thornburg
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ORGANISM: Oryza sativa
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Best Local Similarity 54.7
Matches 163; Conservative
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EDNESS: double
                                        CITY: Indianapolis
STATE: Indiana
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                                                                                                       46204
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                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08858003
Patent No. 6060234
GENERAL INFORMATION:
APPLICANT: Katz, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Stassi, Diane L.
APPLICANT: Ruan, Xiaoan
APPLICANT: Ruan, Xiaoan
APPLICANT: Reada-Lopez, Ana
APPLICANT: Kakayas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
WHOMER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Sequence; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed; OTHER INFORMATION: fragments having NcoI restriction sites, US-09-197-649-7
                                                                                                                                                                                                                                                                                                                                                                               Length 390;
                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.2%; Score 60; DB 4; Length 390
Best Local Similarity 48.0%; Pred. No. 4.4e-05;
Matches 171; Conservative 0; Mismatches 185; Indels
CURRENT FILING DATE: 1998-11-23
ERRLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
ERRLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1991-08-02
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Abbott Laboratories
100 Abbott Park Rd.
                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Abbott Park
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COM-
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-858-003-1/c
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                                                                                                                                                                                  SEQ ID NO 7
                                                                                                                                                                                                                                                           FEATURE:
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1240 ATGGCCATCCGGCGGCGGTACTCGTTGGCGTCGGCCCAGCGCACGGTGTCGCTCTCCCCC 1299
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47.2%; Pred. No. 7.2e-05;
                                                                  FILING DATE: 16-MMY-1979
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NORDER:
FILING DATE:
NAME: DIABNE:
NAME: DIABNE CASULO
REGISTRATION NUMBER: 4952.US.P2
TELEPHONE: (847)-938:3137
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Job time: 20400.7 secs
                                         JMBER: US/08/858,003
16-MAY-1979
SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/858,
                                                                                                                                                                                                                                                                                                                            TELEFAX: (847)-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-858-003-1
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March 26, 2003, 05:23:30 ; Search time 275.743 Seconds
(without alignments)
15433.627 Million cell updates/sec
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5001
1 aggggacactacactttcca......tgccgccggagtgcgcccg 5001
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574371 seqs, 425486471 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Query	:			
Score	Match	Length DB	BB	ID	Description
121.8	2.4	5757	10	US-09-993-170-56	Sequence 56, Appl
118.4	2.4	949	10	US-09-770-445-342	Sequence 342, App
114.4	2.3	547	σ	US-10-101-464A-374	Sequence 374, App
111.2	2.5	2000	10	US-09-887-576-870	Sequence 870, App
83.2	1.7	2000	10	US-09-887-576-859	Sequence 859, App
68.2	1.4	520	σ	US-10-184-644-332	Sequence 332, App
61	1.2	863	10	US-09-974-300-5249	Sequence 5249, Ap
9.09	1.2	15872	σ	US-09-860-846-1	Sequence 1, Appli
60.6	1.2	15872	10	US-09-861-289-1	Sequence 1, Appli
09	1.2	390	10	US-06-190-399-7	Sequence 7, Appli
9	1.2	925	σ	US-09-735-056-1	Sequence 1, Appli
58	1.2	615	თ	US-10-125-815-4	Sequence 4, Appli
57.4	۲.۲	2010	12		Sequence 9, Appli
56.4	1.1	405	10		Sequence 3891, Ap
55.2	1.1	2087	10	US-09-349-385-11	Sequence 11, Appl
54	1.1	264	10	US-09-969-373-472	Sequence 472, App
54	1.1	2000	10	US-09-887-576-832	Sequence 832, App
53.2	1.1	4689	σ	US-09-860-846-34	Sequence 34, Appl
53.2	1.1	4689	10	US-09-861-289-34	Seguence 34, Appl

RESULT 2 US-09-770-445-342

Sequence 30, Appl. Sequence 5, Appli. Sequence 5, Appli. Sequence 4, Appli. Sequence 4, Appli. Sequence 7, Appli. Sequence 32, Appl. Sequence 32, Appl. Sequence 32, Appl. Sequence 7, Appl. Sequence 3, Appl. Sequence 36, Appl. Sequence 832, Appl. Sequence 86, Appl. Sequence 861, Appl. Sequence 861, Appl.	Resistance Gene	Length 5757; Indels 2; Gaps 1; CTATATATTGTAGC 4456 [11 1 1 1 1 1 1 1 1 1
US-09-860-846-30 US-09-861-289-30 US-09-861-289-5 US-09-861-289-5 US-09-861-289-5 US-09-748-033-4 US-09-748-033-4 US-09-748-033-4 US-09-861-289-3 US-09-861-289-3 US-09-861-289-3 US-09-861-289-3 US-09-815-242-7773 US-09-815-242-7773 US-09-815-242-7775 US-09-815-242-7775 US-09-815-242-7775 US-09-815-242-7775 US-09-815-242-7775 US-09-815-242-7775 US-09-815-242-775-832 US-09-815-242-777-875-875-875-875-875-875-875-875-875	ALIGNMENTS 93170 on of a Plant Disease ty and Method for Eng ty 709/993,170 26 48,335	Score 121.8; DB 10; Pred. No. 3.1e-20; 0; Mismatches 22; AdaaGaGaGAATAGCAGGGA
133842 10 36778 9 36778 9 36778 9 1294 9 11220 10 11220 10 11220 10 11220 10 1248 9 113613 10 13613 10	cation US/099931 148004A1 NN: Barbara N: Barbara N: Modification N: Specificity N: Specificity SPC: 2001-11-26 TE: 2001-11-26 TE: 2001-11-26 TE: 2001-11-36 TE: 2001-11-36 TE: 2001-11-36 TE: 2001-11-36 TE: 2001-11-36	2.4%; 86.0%; vative AGAGATAAA,
	(i.cai 2014) 11t, 1 11t, 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	the similarity 147; Conservance on servance on servance on servance of the ser
0 0	SULT 1 -09-993-170-56 Sequence 56, Applic Breath to US200201 Breath INFORMATION APPLICANT: Valent, APPLICANT: PAPAN, TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION FILE REFERENCE: BE CURRENT APPLICATION FILE REPERENCE: DAY FILE REPERENCE: BE CURRENT FILING DATE: RUMBER OF SEQ ID N SOFTWARE: MICROSOF SEQ ID NO 56 IRNGTH: 5757 TYPE: DNA ORGANISM: OTYZE S: 09-993-170-56	Match Local Sines 147; 197 AAACA
0 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SULT 1 Suchen Patent Patent Patent APPLI APPLI APPLI TITLE T	Querry Best Match 43 33 44 44
	R S D C C C C C C C C C C C C C C C C C C	

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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Higgins, Colleen
APPLICANT: Higgins, Colleen
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPERENCE: 11000.10202
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2000-11-01
FRIOR FILING DATE: 1999-01-12
FRIOR FILING DATE: 1999-01-12
FRIOR APPLICATION NUMBER: 09/228,986
FRIOR APPLICATION NUMBER: 60/162,866
FRIOR APPLICATION NUMBER: 60/162,866
FRIOR APPLICATION NUMBER: FUT/US/0000024
FRIOR APPLICATION NUMBER: PUT/US/0000024
FRIOR PILING DATE: 1999-11-01
FRIOR FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1183 ACCTGGATGAGGAGAAGGTGTGGCATGGCGAGATCGGCGCGCGGGGTTGCGGACGACGATG 1242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 ATATTCTTGTAGAGTGTGCTGTCCTTTTCCTTTTGATCGCGGTACCTCCAATGGCA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 114.4; DB 9;
Pred. No. 4.2e-19;
0; Mismatches 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 989
SOFWARE FRACED for Windows Version 4.0
SEQ ID NO 374
LENGTH: 547
                                                                      Sequence 374, Application US/10101464A Publication No. US20030046728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.3%;
Best Local Similarity 52.9%;
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                                                  JS-10-101-464A-374/C
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US-09-887-576-870/C
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US-10-101-464A-374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1423 CAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAG-----GAGGGCGTTAGCG 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1477 AAGGACATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGCGGC 1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: Thaliana FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FASTSEQ for Windows Version 4.0
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Sequence 342, Application US/09770445
                                                                                                                                                                                                                                      Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                       An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                            Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed
TITLE OF INVENTION: thallana
                      Patent No. US20020023281A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
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SEQ ID NO 342
LENGTH: 949
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GTAGGACCAGGTATTAAGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTACATTAA 4560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1206 CATGGCGAGATCGGCGCGCAGGTTGCGGACGAGCATGGCCATCCGGCGGCGGCGTACTCGTT 1265
                                                                                                                                                                                                                                        4441 ACTATATATTTGTAGCCAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATATGACAA 4500
                                                                                                                                                                                                                                                                                                                          GIGIGACCATATATATATATATACTCCCTCCATATTTAATGTATGACACCGTIGA 1364
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1/C27
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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                                                                                                                               Length 2000;
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SEQ ID NO SEQ ID NOS: 612
LENGTH: 520
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                                                                                                                               Score 83.2; DB 10;
Pred. No. 1.2e-10;
                                                                                                                                                                      0; Mismatches
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Publication No. US20030044930A1
GENERAL INFORMATION:
                                                                                                                               1.7%;
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.4%
Best Local Similarity 20.1%
Matches 88; Conservative
                                                                                                                             Query Match
Best Local Similarity 69.65
Matches 128; Conservative
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Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                       TYPE: DNA
CRGANISM: Oryza sativa
US-09-887-576-859
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; ORGANISM: Homo Sapien
US-10-184-644-332
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US-10-184-644-332
                          LENGTH: 2000
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APPLICANT:
APPLICANT:
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APPLICANT:
    SEQ ID NO 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                               APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: ADU, T.
APPLICANT: Han, T.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
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APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 2000;
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Pred. No. 7.4e-18;
0; Mismatches 33;
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CURRENT APPLICATION NUMBER: US/99/887,576
CURRENT PILLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                             FILE REFERENCE: 1360.001051
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
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APPLICANT: Budworth, P. APPLICANT: Brown, D.
Sequence 870, Application US/09887576 Patent No. US20020144047Al GENERAL INFORMATION:
APPLICANT: Budworth, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4555 CATTAACTAT-GATGATTTGGAGC 4577
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Best Local Similarity 81.4%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
COCANISM: Oryza sativa
US-09-887-576-870
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Best Local Similarity
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LENGTH: 2000
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1565 GGGAGAGGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGGGGAACCATGCCGTCCCAGT 1624
us/09860846
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                                                                                                                                                                                                                                                                                                                                                         1625 GGGACCCCACCACGCCCCGC 1645
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Best Local Similarity 45.5%;
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 CGCTGATGCCGATGCNGACGC
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Patent No. US20020164742A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Sherman, D.H.
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Best Local Similarity
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US-09-860-846-1/c
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APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Expression; FILE REPERANCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05; PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PILING DATE: 2001-10-05
PRIOR PILING DATE: 2001-03-05
PRIOR PILING DATE: 2001-03-05
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APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 0.00039;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT PILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OS SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
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PRIOR FILING DATE: 1998-11-23
PRIOR APPLICATION WUMBER: 07/829,461
PRIOR PILLING DATE: 1992-01-31
PRIOR APPLICATION NUMBER: 07/739,055
PRIOR PRIOR DATE: 1991-08-01
PRIOR APPLICATION NUMBER: 07/561,968
PRIOR PILING DATE: 1990-06-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09735056 Publication No. US20030013662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 100 Abbott
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-735-056-1/c
                                                                                                                                                                                                                           LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                               US-09-790-399-7
                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                              FEATURE:
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APPLICANT: Tuerk, Craig
APPLICANT: Fribnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXO2/C1-CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1567 GAGAGGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGGGGGAACCATGCCGTCCCAGTGG 1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1447 AACTGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGACATCCCGGGGCCGGACCGCAGGTG 1506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                      TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE PERERRACE: 600.438021
CURRENT PEPLICATION NUMBER: 02/09/861,289
CURRENT FILIAG DATE: 2001-05-18
PRIOR PEPLICATION NUMBER: 09/105,537
PRIOR PELIAGATION NUMBER: 09/105,537
PRIOR PELIAGATION DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FESTERQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60.6; DB 10;
Pred. No. 0.00039;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/790,399
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/197,649
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA CRGANISM: Streptomyces venezuelae US-09-861-289-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09790399
Patent No. US20020038000A1
GENERAL INFORMATION:
                    Sequence 1, Application US/09861289 Patent No. US20020110897A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 45.5 Matches 216; Conservative
                                                            GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-790-399-7
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1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGGCCCAGCGCTGTCGCTCTCCCCCTGG 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: Description of Artificial Sequence: Sequence INFORMATION: having a 120 repeat of ACG flanked by fixed INFORMATION: fragments having NcoI restriction sites.
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APPLICANT: Stassi, Diane L.
APPLICANT: Sunmers Jr., Richard G.
APPLICANT: Rann, Xiaoan
APPLICANT: Rann, Xiaoan
APPLICANT: Rakavas, Stephan J.
ATILE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES: 34
                                                                                                                                         Length 390;
                                                                                                                                             Query Match 1.2%; Score 60; DB 10; Length 39 Best Local Similarity 48.0%; Pred. No. 3.3e-05; Matches 171; Conservative 0; Mismatches 185; Indels
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PRIOR APPLICATION NUMBER: 60/158,305
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASLSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 615
                                                                                                                                                                                                                                                           Query Match 1.2%;
Best Local Similarity 48.2%;
Matches 163; Conservative (
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                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                            FEATURE: OTHER INFORMATION: megKS6
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0
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Pred. No. 6.4e-05;
0; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hu, Zhihao
APPLICANT: McDaniel, Robert
APPLICANT: Santi, Daniel V.
TITLE OF INVENTION: RECOMBINANT POLYKETIDE SYNTHASE GENES
FILE REFERENCE: 300622004720
CURRENT APPLICATION NUMBER: US/10/125,815
CURRENT FILING DATE: 2002-07-25
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                                                us/09/735,056
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 6//190,024
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                           NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/858,003
FILING DATE:
      FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10125815
Patent No. US20020173008A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 47.2%;
Matches 183; Conservative C
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: uucleic acid
STRANDEDNESS: double
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-09-735-056-1
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GENERAL INCORMATION:
APPLICANT: Addre R. Abad
APPLICANT: Addre R. Abad
APPLICANT: Micholas B. Duck
APPLICANT: And Freq
APPLICANT: Abang Freq
APPLICANT: Annangen
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Desticidal Activity Against Coleopterans
TITLE OF INVENTION: 2010-10-33
FILE REFERENCE: 2001-10-33
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
LEMANDE: 2010
                                                                                                                 1316 CGCCGATGCGGCCGCCGGTCTCGAGGGCGACCTGGAGCGGCGGACGAGATCGGAGTAGA 1375
                                                                                                                                                                                                                                                                                                                                                           CGATGACAGGGAACTGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGACATCCCGGGACCGA 1495
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                                                            Gaps
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                                                        0;
Score 58; DB 9; Length 615;
Pred. No. 0.00015;
0; Mismatches 175; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 CGGTGCCGTGGGCCTCGACTCCGACGTCGCCGCCC 161
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COTHER INFORMATION: (1)...(2010)
COTHER INFORMATION: Maize optimized Cryl218-1
NAME/KEY: misc_feature
LOCATION: (0)...(0)
COTHER INFORMATION: mol218-1
US-10-032-717-9
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1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCCTGGAGCGGCGGACG 1362
                                                                                      1363 AGATOGGAGTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCG 1422
                                                                                                                                                                                  1423 CAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGAC 1482
                                                                                                                                                                                                                                                                              1483 ATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGCGGCTCGTGG 1542
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                                                                                                                                                                                                                              225 geecceacececceccearenageerrergagregageccarecegeegeccreare 166
                                                                                                                                                                                                                                                                                                                         165 ATGTCGTAAACAATGCCGGAGGACCATGAAGTAGGTGAGGAGGAGGAGGGCGAAGACG 106
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                            949 GTCGATGACGCCACGGACGAAGGTCTGGACGCGCGCCACGACGCGCCCCCCGGGGT
                                                                                                                                    285 CCGGAGGAGGCCCTCGATGATGTACTGGCCGTTGACGCGGCCGGACATGAAGACGACG
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TITLE OF INVENTION: PLANTS HAVING SEEDLESS FRUIT
FILE PREFERENCE: MEI-0002
CURRENT APPLICATION NUMBER: US/09/349,385
CURRENT FILING DATE: 1999-07-09
FRALIER APPLICATION NUMBER: 60/115,967
EARLIER FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55.2; DB 10;
Pred. No. 0.002;
0; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09349385
Patent No. US20020152495A1
GENERAL INFORMATION:
APPLICANT: Ito, Toshiro
APPLICANT: Fromm, Michael
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ilarity 44.9%;
Conservative
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Best Local Similarity
Matches 210; Conserva
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US-09-349-385-11/c
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thomson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REPERBYCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: 05/09/878,574
CURRENT APPLICATION NUMBER: 09/333,535
PRIOR PLILING DATE: 2001-12-21
PRIOR FILLING DATE: 1999-06-14
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                                                                                                       1208 IGGCGAGAICGGCGCGCAGGTIGCGGACGAGCAIGGCCAICCGGCGGGGGGGGTACICGIIGG 1267
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                                                              0;
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                   Length 2010;
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                                                            0; Mismatches 286; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA;
; ORGANISM: Glycine max;
; OTHER INFORMATION: Clone ID: LIB3028-004-Q1-B1-E11
US-09-8776-574-3891
                DB 12,
                Score 57.4; DB 12
Pred. No. 0.00054;
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                1.18;
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Similarity 47.58;
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SEQ ID NO 3891
LENGTH: 405
                                                            Matches 229; Conservative
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                                      Similarity
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US-09-878-574-3891/c
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Best Local
                Query Match
                                           Local
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